

Sat Mar 16 13:37:58 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on: March 15, 2002, 14:21:21 ; Search time 63.84 Seconds
(without alignments)
25.204 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKQOFFGLM 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	61	100.0	72	Q9Y494	Q9Y494 homo sapien
2	61	100.0	114	Q97947	Q97947 tupala bela
3	61	100.0	128	Q9Y6V5	Q9Y6V5 homo sapien
4	61	100.0	129	Q97948	Q97948 tupala bela
5	53	86.9	97	Q9Z0K2	Q9Z0K2 cavia porce
6	53	86.9	115	Q9Z0K1	Q9Z0K1 cavia porce
7	53	86.9	130	Q9Z0K0	Q9Z0K0 cavia porce
8	41	67.2	207	Q9HLY7	Q9HLY7 thermoplasma
9	39	63.9	786	Q24014	Q24014 dictyosteli
10	39	63.9	803	Q24012	Q24012 dictyosteli
11	38	62.3	205	Q20174	Q20174 caenorhabdi
12	38	62.3	235	Q9V6W4	Q9V6W4 drosophila
13	38	62.3	257	Q9SUN5	Q9SUN5 arabidopsis
14	38	62.3	293	Q049561	Q049561 arabidopsis
15	38	62.3	496	Q9PVE8	Q9PVE8 fundulus he
16	38	62.3	500	Q9DE99	Q9DE99 oryzias lat
17	38	62.3	502	Q98T91	Q98T91 oryzias lat
18	38	62.3	3722	P94873	P94873 lysobacter
19	37	60.7	138	O84949	O84949 salmonella

20	37	60.7	249	1	Q9V2N2	Q9V2N2 pyrococcus
21	36	59.0	177	5	Q9BPN9	Q9BPN9 caenorhabdi
22	36	59.0	236	5	Q9NEW8	Q9NEW8 caenorhabdi
23	36	59.0	352	12	Q86283	Q86283 unidentified
24	36	59.0	373	10	O23876	O23876 oryza sativ
25	36	59.0	477	3	Q9UW05	Q9UW05 clavispora
26	36	59.0	550	5	Q94130	Q94130 caenorhabdi
27	36	59.0	629	5	O45273	O45273 caenorhabdi
28	36	59.0	869	2	Q9F634	Q9F634 stigmatella
29	35	57.4	128	11	Q99N14	Q99N14 mus musculu
30	35	57.4	206	5	O61761	O61761 caenorhabdi
31	35	57.4	218	2	Q9LSY0	Q9LSY0 streptomyce
32	35	57.4	296	10	Q9LW26	Q9LW26 arabidopsis
33	35	57.4	297	2	Q9HV29	Q9HV29 pseudomonas
34	35	57.4	347	10	Q40055	Q40055 hordeum vul
35	35	57.4	424	10	O48648	O48648 adiantum ca
36	35	57.4	494	2	Q9C117	Q9C117 lactococcus
37	35	57.4	497	2	Q9A0V7	Q9A0V7 streptococc
38	35	57.4	509	12	O65191	O65191 african swi
39	35	57.4	521	5	Q18014	Q18014 caenorhabdi
40	35	57.4	681	5	Q9GUT4	Q9GUT4 leishmania
41	35	57.4	682	11	Q9ESL2	Q9ESL2 cavia porce
42	35	57.4	832	2	P74619	P74619 synechocyst
43	35	57.4	1043	5	Q9XTZ0	Q9XTZ0 caenorhabdi
44	35	57.4	1278	4	Q9UPP5	Q9UPP5 homo sapien
45	35	57.4	1611	10	Q9SDB6	Q9SDB6 arabidopsis

ALIGNMENTS

RESULT 1
ID Q9Y494 PRELIMINARY; PRT; 72 AA.
AC Q9Y494; (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 17, Last annotation update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD, AND BRAIN;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.:
RT "Identification of a Delta isoform of preprotachykinin mRNA in Human
Mononuclear Phagocytes and Lymphocytes."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050657; AAC15703.1;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT NON_TER 1 72
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 8274 MW; 2C02B2BA1EAAD16 CRC64;

Query Match 100.0%; Score 61; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 RPKQOFFGLM 11
Db 23 RPKQOFFGLM 33

RESULT 2
Q97947 PRELIMINARY; PRT; 114 AA.
ID Q97947

```

AC Q97947;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ I.
OS Tupaia belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupalidae; Tupaia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Heitland A., Maegert H.J., Kruhoefter M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50785; CAA90648.1; -
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PRODOM; PD005598; Protachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 83 92 NEUROKININ A.
SQ SEQUENCE 114 AA; 13281 MW; B439C3D27FD47CAB CRC64;

Query Match 100.0%; Score 61; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
DB 58 RPKPQQFFGLM 68

RESULT 3
ID Q9Y6V5 PRELIMINARY; PRT; 128 AA.
AC Q9Y6V5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE WUGSC:H.DJ0841B21.1 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalicki J., Angell S.;
RT "The sequence of Homo sapiens PAC clone DJ0841B21.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004140; AAC02754.1; -
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 1.
SQ SEQUENCE 128 AA; 14770 MW; 0F8D61774AFEC1CA CRC64;

Query Match 100.0%; Score 61; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
DB 58 RPKPQQFFGLM 68

us-09-988-792-1.rspt

Db 58 RPKPQQFFGLM 68

RESULT 4
ID Q97948 PRELIMINARY; PRT; 129 AA.
AC Q97948;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Tupaia belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupalidae; Tupaia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Heitland A., Maegert H.J., Kruhoefter M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50786; CAA90649.1; -
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PRODOM; PD005598; Protachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 129 AA; 14941 MW; 5855E7ADC2D8674E CRC64;

Query Match 100.0%; Score 61; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
DB 58 RPKPQQFFGLM 68

RESULT 5
ID Q920K2 PRELIMINARY; PRT; 97 AA.
AC Q920K2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DELTA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRIN;
RA Heitland A., Maegert H.J., Kruhoefter M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50782; CAA90645.1; -
DR InterPro; IPR003580; Protachykinin.
DR PRODOM; PD005598; Protachykinin; 1.
FT CHAIN 58 68 SUBSTANCE P.
SQ SEQUENCE 97 AA; 11222 MW; FFD50C3297E3F7E3 CRC64;

Query Match 86.98%; Score 53; DB 11; Length 97;
Best Local Similarity 90.98%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

```

```

Db 58 RPKPQQSFGLM 68
||||| ||||
RESULT 6
Q920K1 PRELIMINARY; PRT; 115 AA.
AC Q920K1
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50783; CAA90646.1;
DR InterPro; IPR002040; Tachykinin.
DR ProDom; PD003598; Protachykinin.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 83 92 NEUROKININ A.
SQ SEQUENCE 115 AA; 13190 MW; 39EFFB8CB47174 CRC64;

Query Match 86.9%; Score 53; DB 11; Length 115;
Best Local Similarity 90.9%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQSFGLM 11
||||| ||||
Db 58 RPKPQQSFGLM 68

RESULT 7
Q920K0 PRELIMINARY; PRT; 130 AA.
AC Q920K0
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50784; CAA90647.1;
DR InterPro; IPR002040; Tachykinin.
DR ProDom; PD003598; Protachykinin.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 130 AA; 14850 MW; C4B2F55B6A60A7C0 CRC64;

Query Match 86.9%; Score 53; DB 11; Length 130;
Best Local Similarity 90.9%; Pred. No. 0.018;

QY 1 RPKPQQSFGLM 11
||||| ||||
Db 58 RPKPQQSFGLM 68

RESULT 8
Q9HLY7 PRELIMINARY; PRT; 207 AA.
AC Q9HLY7
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN TA0086.
GN TA0086.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaaceae;
OC Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretka K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum."
RL Nature 407:508-513(2000).
DR EMBL; AL445063; CAC11234.1;
DR InterPro; IPR001279; Beta_lactam_met.
DR Pfam; PF00753; lactamase_B; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 207 AA; 22741 MW; 60136F482EB2A94D CRC64;

Query Match 67.2%; Score 41; DB 1; Length 207;
Best Local Similarity 70.0%; Pred. No. 5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKPQQSFGLM 11
||||| ||||
Db 100 PKPRSFGLM 109

RESULT 9
Q24014 PRELIMINARY; PRT; 786 AA.
AC Q24014
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE GI-LIKE ORF S PRODUCT.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DMUC2;
RX MEDLINE=94302132; PubMed=8029320;
RA Kiyosawa H., Hughes J.E., Welker D.L.;
RT "Compatible Dictyostelium mucoroides nuclear plasmids Dmp1 and Dmp2
RT both belong to the Ddpl plasmid family."
RL Plasmid 31:121-130(1994).
DR EMBL; U00176; AAC14374.1;
SQ SEQUENCE 786 AA; 90191 MW; 2167146E1F012003 CRC64;

Query Match 63.9%; Score 39; DB 5; Length 786;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQSFGLM 10

```

Db 717 KPPIQFFGI 726
 :!:-! !!!!!

RESULT 10
 Q24012 ID Q24012 PRELIMINARY; PRT; 803 AA.
 AC Q24012;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE G1-LIKE ORF'S PRODUCT.
 OS Dictyostellium mucoroides (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
 OX NCBI_TaxID=31287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DMUC2;
 RX MEDLINE=94302132; PubMed=8029320;
 RA Kiyosawa H., Hughes J.E., Welker D.L.;
 RT "Compatible Dictyostellium mucoroides nuclear plasmids Dmpl and Dmp2
 both belong to the dopl plasmid family";
 RL Plasmid 31:121-130(1994).
 DR EMBL; U00175; AAC14372.1; -;
 SQ SEQUENCE 803 AA; 91385 MW; 219f8272f416f6acd CRC64;

Query Match 63.9%; Score 39; DB 5; Length 803;
 Best Local Similarity 60.0%; Pred. No. 49;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 :!:-! !!!!!
 Db 734 KPPIQFFGI 743

RESULT 11
 Q20174 ID Q20174 PRELIMINARY; PRT; 205 AA.
 AC Q20174;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE COSMID F38E9.
 GN F38E9.4
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 Thierly-Mieg J., Thomas K., Vaughan K., Vaughan K., Waterston R.,
 Watson A., Weinstock L., Wilkinon-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP Wu X., Gattung S.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RP Waterston R.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U46668; AAA93346.1; -;
 SQ SEQUENCE 205 AA; 23000 MW; B99f8b37db706ec0d CRC64;

Query Match 62.3%; Score 38; DB 5; Length 205;
 Best Local Similarity 85.7%; Pred. No. 18;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPKPQOFF 8
 :!:-! !!!!!
 Db 151 KPPIQFF 157

RESULT 12
 Q9VBW4 ID Q9VBW4 PRELIMINARY; PRT; 235 AA.
 AC Q9VBW4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE CG13653 PROTEIN.
 GN CG13653.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Bruchycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.F., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Canter A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iyegwan C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Sinden-Klamis I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Zhang G., Zhao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "the genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003751; AAF56413.1; -;
 DR FlyBase; FBgn0039288; CG13653.
 SQ SEQUENCE 235 AA; 27051 MW; FD9BDB4555BA7A3E CRC64;

MEDLINE=37382427; PubMed=95240431;
 Celderer M., Stegeman J.J.;
 RT "Isolation of a cytochrome P450 3A cDNA sequence (CYP3A30) from the
 RT marine teleost Fundulus heteroclitus and phylogenetic analyses of
 RT CYP3A genes";
 RL Biochem. Biophys. Res. Commun. 236:306-312(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Celderer M., Hegelund-Myrback T., Stegeman J.J.;
 RT "Cloning and sequencing of the complete coding region of cytochrome
 RT P450 3A30 (CYP3A30) from the marine teleost Fundulus heteroclitus.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
 CC OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AF105068; AAF1417.1; -
 DR InterPro; IPR001128; Cyt_p450.
 DR Pfam; PF00067; p450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;

KW Monoxygenase; Oxidoreductase.
SQ SEQUENCE 496 AA; 57051 MW; 40CFB23D75F4A4EB CRC64;

Query Match 62.3%; Score 38; DB 13; Length 496;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PRPQOFFGLM 11
 | | | | | | |
Db 40 PRVPFFGTM 49

Search completed: March 15, 2002, 14:30:57
Job time: 576 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:23:11 ; Search time 20.4 Seconds
(without alignments)
19,770 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RRPQOFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	61	100.0	11	TKNA_HORSE	P01290 equus cabal
2	61	100.0	115	TKNI_RABIT	P41540 oryctolagus
3	61	100.0	129	TKNI_HUMAN	P20366 homo sapien
4	61	100.0	130	TKNI_BOVIN	P01289 bos taurus
5	61	100.0	130	TKNI_MESAU	Q60541 mesocricetu
6	61	100.0	130	TKNI_MOUSE	P41539 mus musculus
7	61	100.0	130	TKNI_RAT	P06767 rattus norv
8	58	95.1	11	TKNA_CHICK	P13850 gallus gall
9	50	82.0	11	TKNA_ONCMY	P28499 oncorhynch
10	49	80.3	11	TKNA_GADMO	P28498 gadus morhu
11	48	78.7	11	TKNA_SCYCA	P41333 scylliorhinu
12	44	72.1	11	TKNA_PSEGU	P42989 pseudophryn
13	44	72.1	11	TKN5_PSEGU	P42990 pseudophryn
14	44	72.1	12	TKNI_KASMA	P08613 kassina mac
15	43	70.5	11	TKNA_RANCI	P29207 rana ridibu
16	41	67.2	11	TKNA_RANCA	P22688 rana catesb
17	41	67.2	3828	TRX_DROVI	Q24742 drosophila
18	37	60.7	11	TKNI_UPERU	P08612 uperoleia r
19	37	60.7	11	TKN2_PSEGU	P42987 pseudophryn
20	36	59.0	11	TKN1_PSEGU	P42986 pseudophryn
21	36	59.0	11	TKN3_PSEGU	P42988 pseudophryn
22	36	59.0	12	TKN2_KASMA	P08614 kassina mac
23	36	59.0	12	TKN_KASSE	P08611 kassina sen
24	36	59.0	167	SERO_GALME	Q76192 galleria me
25	36	59.0	313	ISPE_HAEIN	P45271 haemophilus
26	36	59.0	728	EF2_ARCFU	Q28385 archaeoglob
27	35	57.4	512	SYK_VIBCH	Q9ku60 vibrio chol
28	35	57.4	518	CP3R_ONCMY	Q42563 oncorhynch
29	35	57.4	757	RELA_MYXXA	O52177 myxococcus
30	35	57.4	1092	DP2L_METHH	O27579 methanobact
31	34	55.7	493	Y130_MYCPN	P75506 mycoplasma
32	34	55.7	498	C6B1_PAPPO	Q04552 papilio pol
33	34	55.7	503	CP3A_MESAU	Q64148 mesocricetu

34	34	55.7	504	1	CP31_RAT	P04800 rattus norv
35	34	55.7	585	1	PPOE_LYCES	Q08296 lycopersico
36	34	55.7	587	1	PPOE_LYCES	Q08307 lycopersico
37	34	55.7	588	1	PPOB_SOLITU	Q06355 solanum tub
38	34	55.7	666	1	YJ50_YEAST	P47077 saccharomyc
39	34	55.7	1799	1	YO25_CAEEL	P34675 caenorhabdi
40	33	54.1	282	1	YK00_CAEEL	P42001 caenorhabdi
41	33	54.1	404	1	CAG5_CHICK	Q92184 gallus gall
42	33	54.1	420	1	CRF1_CHICK	Q90812 gallus gall
43	33	54.1	495	1	SYK_STAAU	O53638 staphylococ
44	33	54.1	498	1	C6B3_PAPPO	Q27756 papilio pol
45	33	54.1	501	1	SYK_PASMU	P57822 pasteurella

ALIGNMENTS

```
RESULT 1
TKNA_HORSE
ID TKNA_HORSE STANDARD; PRT; 11 AA.
AC P01290:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Equus caballus (Horse), and Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796, 10141;
RN [1]
RP SEQUENCE.
RC SPECIES=Horse;
RA Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
   intestine.";
RL Helv. Chim. Acta 56:860-866(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C. porcellus;
RX MEDLINE=90044685; PubMed=2478925;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P.";
RL Neuropeptides 14:105-110(1989).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
   EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
   SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
   MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01558; SPHO.
DR PIR; A60654; A60654.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuroptide; Amidation; Neurotransmitter.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;
```

Query Match 100.0%; Score 61; DB 1; Length 11,
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOFFGLM 11
Db 1 RRPQOFFGLM 11

RESULT 2
TKNI_RABIT STANDARD; PRT; 115 AA.

AC P41540;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ I PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE GAMMA; C-TERMINAL
 DE FLANKING PEPTIDE]
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93371392; PubMed=8363593;
 RA Maedert H.J., Heitland A., Rose M., Forssmann W.G.;
 RT "Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.";
 RL Biochem. Biophys. Res. Commun. 195:128-131(1993).
 RN [2]
 RP SEQUENCE OF 72-92.
 RA Rago R., McGregor G.P., Thim L., Conlon J.M.;
 RT "Gamma-neuropeptide K: a peptide isolated from rabbit gut that is
 RT derived from gamma-preprotachykinin.";
 RL Regul. Pept. 18:346-346(1987).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X62994; CAA44728.1;
 DR PIR; S18922; S18922.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR Prodom; PD005598; Protachykinin; 1.
 DR SMART; SM00203; TK; 2.
 DR PROSITE; PS00267; TACHYKININ; 2.
 KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19
 FT PEPTIDE 20 56 POTENTIAL.
 FT PEPTIDE 58 68 SUBSTANCE P.
 FT PEPTIDE 72 92 NEUROPEPTIDE GAMMA.
 FT PEPTIDE 83 92 NEUROKININ A.
 FT PEPTIDE 96 111 C-TERMINAL FLANKING PEPTIDE.
 FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD_RES 92 92 AMIDATION (G-93 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 115 AA; 13370 MW; 5EC76F7C9B10E1C6 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQOFGFLM 11
 |||||
 Db 58 RPKPQOFGFLM 68
 |||||

RESULT 3
 TKNI_HUMAN

TKNI_HUMAN STANDARD; PRT; 129 AA.
 P20366; O00072; O60600; O60601;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ I PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE]
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RX MEDLINE=87030957; PubMed=3770210;
 RA Harnar A.J., Armstrong A., Pascall J.C., Chapman K., Kosic R.,
 RA Curtis A., Goring J., Edwards C.R.W., Fink G.;
 RT "cDNA sequence of human beta-preprotachykinin, the common precursor
 RT to substance P and neurokinin A.";
 RL FEBS Lett. 208:67-72(1986).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC TISSUE=Brain;
 RA Tan A., Too H.P.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases
 RN [3]
 RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE=Testis.
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chivakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
 RA Ivell R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 RT human and mouse testis.";
 RL Endocrinology 128:2441-2448(1991).
 RN [4]
 RP SEQUENCE OF 98-107.
 RX MEDLINE=87275962; PubMed=3038549;
 RA Theodorsson-Norheim E., Joernvall H., Andersson M., Norheim I.,
 RA Oberg K., Jacobsson G.;
 RT "Isolation and characterization of neurokinin A, neurokinin A(3-10)
 RT and neurokinin A(4-10) from a neutral water extract of a metastatic
 RT ileal carcinoid tumour.";
 RL Eur. J. Biochem. 166:693-697(1987).
 RN [5]
 RP SEQUENCE OF 36-118 FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Blood, and Brain;
 RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
 RT "Identification of a delta isoform of preprotachykinin mRNA in human
 RT mononuclear phagocytes and lymphocytes.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 111-126.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=91133994; PubMed=2284201;
 RA McGregor G.P., Conlon J.M.;
 RT "Characterization of the C-terminal flanking peptide of human
 RT beta-preprotachykinin.";
 RL Peptides 11:907-910(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

or send an email to license@lsb-sib.ch).

```

CC EMBL: X54469; CAA38351.1; -
CC EMBL: U37529; AAA79195.1; -
CC EMBL: M68906; AAA60159.1; -
CC EMBL: M68907; AAA60160.1; -
CC EMBL: AF050656; AAC15702.1; -
CC EMBL: AF050658; AAC15704.1; -
CC PIR: A24805; A24805.
CC PIR: S00069; S00069.
CC MIM: 162320; -
CC InterPro: IPR003580; Protachykinin.
CC InterPro: IPR002040; Tachykinin.
CC Pfam: PF02202; Tachykinin; 1.
CC ProDom: PD005598; Protachykinin; 1.
CC SMART: SM00203; TK; 2.
CC PROSITE: PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE K.
FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 98 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE.
FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM DELTA).
FT VARSPPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM DELTA).
FT VARSPPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM DELTA).
FT CONFLICT 87 87 L -> P (IN REF. 4).
FT CONFLICT 129 AA; 15003 MW; 51412C1692368DE4 CRC64;
SQ SEQUENCE 129 AA; 15003 MW; 51412C1692368DE4 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQPFGLM 11
Db 58 RPKPQQPFGLM 68

RESULT 4.
TKNL_BOVIN STANDARD; PRT; 130 AA.
AC P01291; P04091; P20773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=85086245; PubMed=6083453;
RA Nawa H., Kotani H., Nakanishi S.;
RT "Tissue-specific generation of two preprotachykinin mRNAs from one
RL gene by alternative RNA splicing.";
RN Nature 312:729-734 (1984).
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).

```

```

RX MEDLINE=84039802; PubMed=6195531;
RA Nawa H., Hirose T., Takashima H., Inayama S., Nakanishi S.;
RT "Nucleotide sequences of cloned cDNAs for two types of tyrosine brain
RT substance P precursor.";
RL Nature 306:32-36 (1983).
RN [3]
RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RC TISSUE-Hypothalamus;
RX MEDLINE=91209287; PubMed=1708336;
RA Chivakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Ivell R.;
RT "Tachykinin (substance-P) gene expression in Leydig cells of the
RT human and mouse testis.";
RL Endocrinology 128:2441-2448 (1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECKETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC
CC EMBL: X00075; CAA24939.1; -
CC EMBL: X00075; CAA24940.1; -
CC EMBL: X00075; CAA24941.1; -
CC EMBL: X00076; CAA24942.1; -
CC EMBL: X00076; CAA24943.1; ALT_SEQ.
CC EMBL: X02351; CAA26206.1; -
CC EMBL: X01396; CAA26206.1; JOINED.
CC EMBL: X01397; CAA26206.1; JOINED.
CC EMBL: X01398; CAA26206.1; JOINED.
CC EMBL: X01399; CAA26206.1; JOINED.
CC EMBL: X01400; CAA26206.1; JOINED.
CC EMBL: M68911; AAA30724.1; -
CC EMBL: M68912; AAA30725.1; -
CC PIR: A01557; SPBOA.
CC PIR: A01559; SPBOB.
CC PIR: A05093; A05093.
CC PIR: B25067; B25067.
CC InterPro: IPR003580; Protachykinin.
CC InterPro: IPR002040; Tachykinin.
CC Pfam: PF02202; Tachykinin; 1.
CC ProDom: PD005598; Protachykinin; 1.
CC SMART: SM00203; TK; 2.
CC PROSITE: PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 POTENTIAL.
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE K.
FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 98 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM DELTA).
FT VARSPPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM DELTA).
FT VARSPPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM DELTA).
FT CONFLICT 121 121 V -> A (IN REF. 3).
FT CONFLICT 130 AA; 15076 MW; CE2A28572305DEB7 CRC64;
SQ SEQUENCE 130 AA; 15076 MW; CE2A28572305DEB7 CRC64;

```


FT PEPTIDE 98 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA).
 SQ SEQUENCE 130 AA; 15045 MW; 7B8DA15FDE72FF8 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQFFGLM 11
 IIIIIIIIII
 Db 58 RPKPQQFFGLM 68

RESULT 7
 TKNL_RAT STANDARD; PRT; 130 AA.
 AC P06767; P08856; P22356;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
 RX MEDLINE=90331040; PubMed=1695945;
 RA Carter M.S., Krause J.E.;
 RT "Structure, expression, and some regulatory mechanisms of the rat
 RT preprotachykinin gene encoding substance P, neurokinin A,
 RT neuropeptide K, and neuropeptide gamma.";
 RL J. Neurosci. 10:2203-2214(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
 RX MEDLINE=87118268; PubMed=2433692;
 RA Krause J.E., Chirgwin J.M., Carter M.S., Xu Z.S., Hershey A.D.;
 RT "Three rat preprotachykinin mRNAs encode the neuropeptides substance
 RT P and neurokinin A.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:881-885(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=87025808; PubMed=2429656;
 RA Kawaguchi Y., Hoshimaru M., Nawa H., Nakanishi S.;
 RT "Sequence analysis of cloned cDNA for rat substance P precursor:
 RT existence of a third substance P precursor.";
 RL Biochem. Biophys. Res. Commun. 139:1040-1046(1986).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX TISSUE=Dorsal root ganglion;
 RC MEDLINE=91085565; PubMed=1702066;
 RA Haimar A.J., Hyde V., Chapman K.E.;
 RT "Identification and cDNA sequence of delta-preprotachykinin, a fourth
 RT splicing variant of the rat substance P precursor.";
 RL FEBS Lett. 275:22-24(1990).
 RN [5]
 RP SEQUENCE OF 1-41 FROM N.A.
 RX MEDLINE=93192337; PubMed=8448217;
 RA Chapman K.E., Lyons V., Haimar A.J.;
 RT "The sequence of 5' flanking DNA from the rat preprotachykinin gene;
 RT analysis of putative transcription factor binding sites.";
 RL Biochim. Biophys. Acta 1172:361-363(1993).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.

CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M34162; AAA41926.1;
 DR EMBL; M34159; AAA41926.1; JOINED.
 DR EMBL; M34160; AAA41926.1; JOINED.
 DR EMBL; M34161; AAA41926.1; JOINED.
 DR EMBL; M34184; AAA41925.1;
 DR EMBL; M34183; AAA41929.1;
 DR EMBL; M15191; AAA41928.1;
 DR EMBL; M14312; AAA41927.1;
 DR EMBL; L07328; AAA41924.1;
 DR EMBL; X56306; CAA39752.1;
 DR PIR; A26590; A26590.
 DR PIR; B26590; B26590.
 DR PIR; C26590; C26590.
 DR PIR; A37163; A37163.
 DR PIR; S12958; S12958.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR ProDom; PD005598; Protachykinin; 1.
 DR SMART; SM00203; TK; 2.
 DR PROSITE; PS00267; TACHYKININ; 2.
 KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 56 SUBSTANCE P.
 FT PEPTIDE 58 68 NEUROPEPTIDE K.
 FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
 FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 2ND PART.
 FT PEPTIDE 89 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM
 FT VARSPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM
 FT VARSPLIC 115 115 DELTA).
 FT VARSPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM
 FT DELTA).
 SQ SEQUENCE 130 AA; 15001 MW; B22EFE860DCCD75A CRC64;

Query Match 100.0%; Score 61; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQFFGLM 11
 IIIIIIIIII
 Db 58 RPKPQQFFGLM 68

RESULT 8
 TKNA_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine; PubMed=2452461;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "(Arg3)substance P and neurokinin A from chicken small intestine.";
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; JN0023.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 DR Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 95.1%; Score 58; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 5e-05;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
 II:IIIIIIII
 DB 1 RRPQOFFGLM 11

RESULT 9
 TKNA_ONCMY STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; S23307; S23308.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 DR Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 82.0%; Score 50; DB 1; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.0015;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
 II:IIIIIIII
 DB 1 KRPPOFFGLM 11

RESULT 10
 TKNA_GADMO STANDARD; PRT; 11 AA.
 AC P28498;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae; Gadidae;
 OC Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 DR Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC54;

Query Match 80.3%; Score 49; DB 1; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.0023;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
 II:IIIIIIII
 DB 1 KRPPOFFGLM 11

RESULT 11
 TKNA_SCYCA STANDARD; PRT; 11 AA.
 AC P41333;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93292508; PubMed=7685693;
 RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;

RT Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, *Scyliorhinus canicula*.²;
 RL Eur. J. Biochem. 214:469-474(1993).

CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.

CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR; S33300; S33300.

DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.

DR Pfam: PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match

Best Local Similarity 78.7%; Score 48; DB 1; Length 11;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

DB 1 KRPFGOFFGLM 11

:|:|:|:|:|

RESULT 12

TKM4_PSEGU

ID TKN4_PSEGU STANDARD; PRT; 11 AA.

AC P42989;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE SUBSTANCE P-LIKE PEPTIDE I (PG-SPI).

OS Pseudophryne guentheri (Frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;

OC Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin;

RX MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of

RT the Australian frog Pseudophryne guntheri.²;

RL Peptides 11:299-304(1990).

CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

CC MUSCLES.

CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR; E60409; E60409.

DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.

DR Pfam: PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match

Best Local Similarity 72.1%; Score 44; DB 1; Length 11;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

:|:|:|:|:|

DB 1 QPNPDEFFGLM 11

RESULT 13

TKM5_PSEGU

ID TKN5_PSEGU STANDARD; PRT; 11 AA.

AC P42990;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE SUBSTANCE P-LIKE PEPTIDE II (PG-SPII).

OS Pseudophryne guentheri (Frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;

OC Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin;

RX MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of

RT the Australian frog Pseudophryne guntheri.²;

RL Peptides 11:299-304(1990).

CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

CC MUSCLES.

CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR; F60409; F60409.

DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.

DR Pfam: PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match

Best Local Similarity 72.1%; Score 44; DB 1; Length 11;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

:|:|:|:|:|

DB 1 QPNPNEFFGLM 11

RESULT 14

TKM1_KASMA

ID TKN1_KASMA STANDARD; PRT; 12 AA.

AC P08613;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE HYLAMBATES KASSININ (GLU(2)-PRO(5) KASSININ).

OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranolia; Hyperoliidae;

OC Kassina.

OX NCBI_TaxID=8414;

RN [1]

RP SEQUENCE.

RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;

RT "New tachykinins, Glu2, pro5-kassinin (hylambates-kassinin) and

RT hylambatin, in the skin of the African rhacophorid frog Hylambates

RT maculatus.²;

RL Biomed. Res. 2:613-617(1981).

CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.

-!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR; S10059; S10059.

DR InterPro; IPR003580; Protachykinin.

DR InterPro; IPR002040; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.

FT MOD_RES 12 12 AMIDATION.

SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;

Query Match

Best Local Similarity 72.1%; Score 44; DB 1; Length 12;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQOFFGLM 11

DB 3 PKPDQFVGLM 12

RESULT 15

TKNA_RANRI

ID TKNA_RANRI STANDARD; PRT: 11 AA.

AC P29207;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE RANAKININ (SUBSTANCE-P-RELATED PEPTIDE).

OS Rana ridibunda (Laughing frog) (Marsh frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8406;

RN 11

RP SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=92044543; PubMed=1658233;

RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;

RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with

neurokinin B from the brain of the frog Rana ridibunda.";

RL J. Neurochem. 57:2086-2091(1991).

CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

MUSCLES.

-!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR InterPro; IPR003580; Protachykinin.

DR InterPro; IPR002040; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match

Best Local Similarity 70.5%; Score 43; DB 1; Length 11;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

DB 1 KPNPERFYGLM 11

Search completed: March 15, 2002, 14:32:18

Job time: 547 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:19:30 ; Search time 32.16 Seconds
(without alignments)
7.697 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKQOFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	1	US-07-934-553-1
2	61	100.0	11	1	US-08-184-935-12
3	61	100.0	11	1	US-08-269-288-2
4	61	100.0	11	1	US-08-338-484-1
5	61	100.0	11	1	US-08-175-432-1
6	61	100.0	11	1	US-08-225-474-1
7	61	100.0	11	1	US-08-391-910-2
8	61	100.0	11	1	US-08-418-994-2
9	61	100.0	11	1	US-08-480-505-3
10	61	100.0	11	1	US-08-391-814-2
11	61	100.0	11	1	US-08-167-870-1
12	61	100.0	11	1	US-08-255-272-6
13	61	100.0	11	1	US-08-441-591-6
14	61	100.0	11	1	US-08-303-362A-6
15	61	100.0	11	1	US-08-462-859A-1
16	61	100.0	11	1	US-08-123-659A-1
17	61	100.0	11	1	US-08-462-415-2
18	61	100.0	11	1	US-08-463-874-2
19	61	100.0	11	1	US-08-464-247A-1
20	61	100.0	11	1	US-08-464-248A-1
21	61	100.0	11	1	US-08-444-135-2
22	61	100.0	11	1	US-08-318-391-2
23	61	100.0	11	2	US-08-796-598-11
24	61	100.0	11	2	US-08-447-175A-11
25	61	100.0	11	2	US-07-737-371E-77
26	61	100.0	11	2	US-08-848-766A-1
27	61	100.0	11	3	US-08-927-128-17

28	61	100.0	11	4	US-08-257-966-2	Sequence 2, Appli
29	61	100.0	11	5	PCT-US95-05600-23	Sequence 23, Appli
30	61	100.0	11	6	5441935-1	Patent No. 5441935
31	61	100.0	12	1	US-08-441-591-7	Sequence 7, Appli
32	61	100.0	12	1	US-08-303-362A-7	Sequence 7, Appli
33	61	100.0	12	4	US-08-505-250-27	Sequence 27, Appli
34	61	100.0	12	4	US-08-505-250-53	Sequence 53, Appli
35	61	100.0	12	5	PCT-US92-06532-4	Sequence 4, Appli
36	61	100.0	12	5	PCT-US95-05600-24	Sequence 24, Appli
37	61	100.0	20	3	US-08-890-157A-2	Sequence 2, Appli
38	61	100.0	20	4	US-08-505-250-50	Sequence 50, Appli
39	61	100.0	126	6	5268359-5	Patent No. 5268359
40	61	100.0	130	6	5268359-2	Patent No. 5268359
41	61	100.0	487	1	US-08-462-859A-9	Sequence 9, Appli
42	61	100.0	487	1	US-08-123-659A-9	Sequence 9, Appli
43	61	100.0	487	1	US-08-464-247A-9	Sequence 9, Appli
44	61	100.0	487	1	US-08-464-248A-9	Sequence 9, Appli
45	61	100.0	492	1	US-08-462-859A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-07-934-553-1
; Sequence 1, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IgE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,553
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-90333CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-934-553-1

Query Match 100.0% Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RPKQOFFGLM 11

TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-484-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQQFFGLM 11
| | | | | | | | | | | | | |
DB 1 RRPQQFFGLM 11

RESULT 5
US-08-175-432-1

; Sequence 1, Application US/08175432
; Patent No. 5495047
; GENERAL INFORMATION:
; APPLICANT: Saari, Walfred S.
; APPLICANT: Van Niel, Monique B.
; APPLICANT: Williams, Brian J.
; TITLE OF INVENTION: FUSED TRICYCLIC COMPOUNDS,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE
; TITLE OF INVENTION: IN THERAPY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORTH, ROBERT J.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,432
FILING DATE: 07-JAN-1994
CLASSIFICATION: 560

ATTORNEY/AGENT INFORMATION:
NAME: NO. 5495047th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1152Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-175-432-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQQFFGLM 11

DB 1 RRPQQFFGLM 11
| | | | | | | | | | | | | |

RESULT 6
US-08-225-474-1

; Sequence 1, Application US/08225474
; Patent No. 5560915
; GENERAL INFORMATION:
; APPLICANT: Patterson, Roy
; APPLICANT: Harris, Kathleen E.
; TITLE OF INVENTION: Method and Composition for Treating
; TITLE OF INVENTION: Ige Mediated Allergies
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION/DOCKET NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000
TELEFAX: (312)-456-7776

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-225-474-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQQFFGLM 11
| | | | | | | | | | | | | |
DB 1 RRPQQFFGLM 11

RESULT 7

US-08-391-910-2
; Sequence 2, Application US/08391910
; Patent No. 5563133
; GENERAL INFORMATION:
; APPLICANT: Hipskind, Philip A.
; TITLE OF INVENTION: HEXAMETHYLENIMINYL TACHYKININ RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PATENTIN RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/08/391,910
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9979
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-910-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 8
US-08-418-994-2
Sequence 2, Application US/08418994
Patent No. 5565568
GENERAL INFORMATION:
APPLICANT: Cho, Sung-Yong S.
APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, J. J.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: 2-ACYLAMINOPROPANAMIDES AS TACHYKININ
RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PATENTIN RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/08/418,994
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-8252

TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-418-994-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 9
US-08-480-505-3
Sequence 3, Application US/08480505
Patent No. 5601821
GENERAL INFORMATION:
APPLICANT: STANWORTH, DENIS R
APPLICANT: LEWIN, IAN V
APPLICANT: NAYYAR, SARITA
APPLICANT: JONES, VALERIE
TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
THEIR USE IN ANTI-ALLERGY TREATMENT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22201-3360
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,505
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/102,692
FILING DATE:
APPLICATION NUMBER: US 07/776,380
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: GB 8913737.6
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB90/00926
FILING DATE: 15-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 875-0400
TELEFAX: (703) 525-3468
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Neuropeptide "Substance P"
US-08-480-505-3

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 10
US-08-391-814-2
; Sequence 2, Application US/08391814
; Patent No. 5607947
; GENERAL INFORMATION:
; APPLICANT: Hiskind, Philip A.
; TITLE OF INVENTION: PYRROLIDINYL TACHYKININ RECEPTOR
; NUMBER OF SEQUENCE: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-391-814-2.

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 11
US-08-167-870-1
; Sequence 1, Application US/08167870
; Patent No. 5610183
; GENERAL INFORMATION:
; APPLICANT: OWENS, ANDREW P.

; APPLICANT: WILLIAMS, BRIAN J.
; TITLE OF INVENTION: AROMATIC COMPOUNDS, COMPOSITIONS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERT J. NORTH
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,870
; FILING DATE: 17-DEC-1993
; CLASSIFICATION: 544
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J.
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: T-1151Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-7262
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-167-870-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 12
US-08-255-272-6
; Sequence 6, Application US/08255272
; Patent No. 5627268
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Sharma, Ajay
; APPLICANT: Khoury-Christianson, Anastasia
; APPLICANT: M.
; TITLE OF INVENTION: Production of Therapeutic Peptides in
; Transgenic Animals as a Fusion with Hemoglobin
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/255,272
FILING DATE: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 6794-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acids
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-255-272-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 13

US-08-441-591-6
Sequence 6, Application US/08441591
Patent No. 5637682

GENERAL INFORMATION:

APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.

TITLE OF INVENTION: HIGH-AFFINITY

TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS

TITLE OF INVENTION: TO THE TACHYKININ

TITLE OF INVENTION: SUBSTANCE P

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,591

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/303,362

FILING DATE: 9-SEPTEMBER-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991

FILING DATE: 8-SEPTEMBER 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 14

US-08-303-362A-6

Sequence 6, Application US/08303362A

Patent No. 5648214

GENERAL INFORMATION:

APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.

TITLE OF INVENTION: HIGH-AFFINITY

TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS

TITLE OF INVENTION: TO THE TACHYKININ

TITLE OF INVENTION: SUBSTANCE P

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,362A

FILING DATE: 9-SEPTEMBER-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991

FILING DATE: 8-SEPTEMBER 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX21

Search completed: March 15, 2002, 14:23:05
Job time: 215 sec

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-362A-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
Db 1 RPKPQOFFGLM 11

RESULT 15
US-08-462-859A-1
; Sequence 1, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
Db 1 RPKPQOFFGLM 11

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:20:56 ; Search time 352.97 seconds
(without alignments)
8.653 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues
Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main.*
1: /cgn2_6/ptodata/2/paa/PTCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	3	US-07-618-504A-2
2	61	100.0	11	3	US-07-618-504A-2
3	61	100.0	11	3	US-07-618-504A-2
4	61	100.0	11	3	US-07-618-504A-2
5	61	100.0	11	3	US-07-618-504A-2
6	61	100.0	11	3	US-07-618-504A-2
7	61	100.0	11	3	US-07-618-504A-2
8	61	100.0	11	3	US-07-618-504A-2
9	61	100.0	11	3	US-07-618-504A-2

10	61	100.0	11	6	US-08-259-266-2	Sequence 2, Appli
11	61	100.0	11	7	US-08-307-741-2	Sequence 2, Appli
12	61	100.0	11	7	US-08-343-750-2	Sequence 2, Appli
13	61	100.0	11	7	US-08-387-056-2	Sequence 2, Appli
14	61	100.0	11	8	US-08-401-394-2	Sequence 2, Appli
15	61	100.0	11	8	US-08-401-394A-2	Sequence 2, Appli
16	61	100.0	11	8	US-08-408-238-2	Sequence 2, Appli
17	61	100.0	11	10	US-08-680-004-17	Sequence 17, Appli
18	61	100.0	11	12	US-08-844-462-11	Sequence 11, Appli
19	61	100.0	11	16	US-09-265-690B-3	Sequence 3, Appli
20	61	100.0	11	16	US-09-265-690C-3	Sequence 3, Appli
21	61	100.0	11	16	US-09-285-387-1	Sequence 1, Appli
22	61	100.0	11	16	US-09-285-387A-1	Sequence 1, Appli
23	61	100.0	11	17	US-09-341-590-112	Sequence 112, App
24	61	100.0	11	17	US-09-394-881-1	Sequence 1, Appli
25	61	100.0	11	18	US-09-428-692-21	Sequence 21, Appli
26	61	100.0	11	18	US-09-489-667A-1	Sequence 1, Appli
27	61	100.0	11	19	US-09-518-550-6	Sequence 6, Appli
28	61	100.0	11	19	US-09-523-790-4	Sequence 4, Appli
29	61	100.0	11	19	US-09-597-734-17	Sequence 17, Appli
30	61	100.0	11	19	US-09-597-734A-17	Sequence 17, Appli
31	61	100.0	11	20	US-09-625-098A-1	Sequence 1, Appli
32	61	100.0	11	20	US-09-629-642A-1	Sequence 1, Appli
33	61	100.0	11	20	US-09-657-276-612	Sequence 612, App
34	61	100.0	11	20	US-09-657-276-625	Sequence 625, App
35	61	100.0	11	20	US-09-657-276-626	Sequence 626, App
36	61	100.0	12	3	US-07-741-200-4	Sequence 4, Appli
37	61	100.0	12	18	US-09-403-752A-41	Sequence 41, Appli
38	61	100.0	12	18	US-09-428-692-22	Sequence 22, Appli
39	61	100.0	12	18	US-09-428-692-25	Sequence 25, Appli
40	61	100.0	12	18	US-09-428-692-28	Sequence 28, Appli
41	61	100.0	12	18	US-09-489-667A-2	Sequence 2, Appli
42	61	100.0	12	18	US-09-489-667A-5	Sequence 5, Appli
43	61	100.0	12	18	US-09-489-667A-8	Sequence 8, Appli
44	61	100.0	12	19	US-09-551-151-41	Sequence 41, Appli
45	61	100.0	12	23	US-09-938-112-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-07-618-504A-2
Sequence 2, Application US/07618504A
GENERAL INFORMATION:
APPLICANT: HOESS, RONALD H
APPLICANT: O BRIEN, JOHN P
APPLICANT: SALEMME, FRANCIS R
TITLE OF INVENTION: STRUCTURAL PROTEINS FROM
ARTIFICIAL GENES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: DU PONT COMPANY
STREET: BARLEY MILL PLAZA 36/2116
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19880-0036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/618,504A
FILING DATE: 19901128
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SIEGELL, BARBARA C
REFERENCE/DOCKET NUMBER: CR 8895
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-892-7949

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-618-504A-2

```

```

Query Match          100.0%; Score 61; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RPKPQQFFGLM 11
   |||||
DB 1 RPKPQQFFGLM 11

```

```

RESULT 2
US-07-670-039A-2
; Sequence 2, Application US/07670039A
; GENERAL INFORMATION:
; APPLICANT: Gerard, Norma P.
; TITLE OF INVENTION: CONTROLLING NK-1 RECEPTOR-
; TITLE OF INVENTION: MEDIATED RESPONSES AND RELATED
; TITLE OF INVENTION: DIAGNOSTICS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/670.039A
; FILING DATE: 19910315
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/062001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-670-039A-2

```

```

Query Match          100.0%; Score 61; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RPKPQQFFGLM 11
   |||||
DB 1 RPKPQQFFGLM 11

```

```

RESULT 3

```

```

US-07-705-071-1
; Sequence 1, Application US/07705071
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING 19E
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/705.071
; FILING DATE: 19910524
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-9033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-705-071-1

```

```

Query Match          100.0%; Score 61; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RPKPQQFFGLM 11
   |||||
DB 1 RPKPQQFFGLM 11

```

```

RESULT 4
US-07-877-675A-5
; Sequence 5, Application US/07877675A
; GENERAL INFORMATION:
; APPLICANT: Vittek Dr., Michael P.
; APPLICANT: Jacobsen Dr., Jack S.
; TITLE OF INVENTION: Novel Amyloid Precursor Proteins and
; TITLE OF INVENTION: Methods of Using Same
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: 1937 West Main Street
; CITY: Stamford
; STATE: CT
; COUNTRY: USA
; ZIP: 06904-0060
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/877.675A
; FILING DATE: 19920501

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 31844-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
TELEFAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-877-675A-5

Query Match 100.0%; Score 61; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
Db 1 RPKPQOFFGLM 11

RESULT 5
US-08-102-875-2
Sequence 2, Application US/08102875
GENERAL INFORMATION:
APPLICANT: HOESS, RONALD H.
APPLICANT: O'BRIEN, JOHN P.
APPLICANT: SALEMME, FRANCIS R.
TITLE OF INVENTION: STRUCTURAL PROTEINS
TITLE OF INVENTION: FROM ARTIFICIAL GENES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5", 1.0 MB
COMPUTER: MAC INTOSH
OPERATING SYSTEM: MAC INTOSH, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,875
FILING DATE: AUGUST 6, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CR-8895
FILING DATE: NOVEMBER 28, 1990
ATTORNEY/AGENT INFORMATION:
NAME: SIEGELL, BARBARA C.
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: CR-8895-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-102-875-2

Query Match 100.0%; Score 61; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
Db 1 RPKPQOFFGLM 11

RESULT 6
US-08-119-244-2
Sequence 2, Application US/08119244
GENERAL INFORMATION:
APPLICANT: Lamberts, Steven W
APPLICANT: Visser, Theofilus J
APPLICANT: Krenning, Eric P
APPLICANT: Bakker, Willem H
APPLICANT: van Hagen, Petrus M
TITLE OF INVENTION: Method for Detecting and Localizing
TITLE OF INVENTION: Tissues Having Neurokinine 1 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mallinckrodt Medical Inc.
STREET: 675 McDonnell Blvd PO Box 5840
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,244
FILING DATE: 09-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91200955.2
FILING DATE: 22-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: McBride, Thomas P
REGISTRATION NUMBER: 32706
REFERENCE/DOCKET NUMBER: 728US/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-895-2414
TELEFAX: 314-895-2156
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-119-244-2

Query Match 100.0%; Score 61; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
Db 1 RPKPQOFFGLM 11

RESULT 7
US-08-153-847-2

```
; Sequence 2, Application US/08153847
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung Y.
; APPLICANT: Crowell, Thomas A.
; APPLICANT: Gitter, Bruce D.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, James J.
; APPLICANT: Krushinski, Joseph H.
; APPLICANT: Lobb, Karen L.
; APPLICANT: Muehl, Brian S.
; APPLICANT: Nixon, James A.
; TITLE OF INVENTION: NON-PEPTIDE TACHYKININ RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Division/PJG
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153.847
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8849
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-153-847-2

Query Match 100.0%; Score 61; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 8
US-08-171-134-2
; Sequence 2, Application US/08171134
; GENERAL INFORMATION:
; APPLICANT: Crowell, Thomas A.
; APPLICANT: Gitter, Bruce D.
; APPLICANT: Jones, Charles D.
; APPLICANT: Lunn, William H.W.
; TITLE OF INVENTION: NON-PEPTIDE TACHYKININ RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171.134
; FILING DATE:
; CLASSIFICATION: 546
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-171-134-2

Query Match 100.0%; Score 61; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 9
US-08-235-401-2
; Sequence 2, Application US/08235401
; GENERAL INFORMATION:
; APPLICANT: Bruns, Robert F.
; APPLICANT: Gitter, Bruce D.
; APPLICANT: Monn, James A.
; APPLICANT: Zimmerman, Dennis M.
; TITLE OF INVENTION: NON-PEPTIDYL TACHYKININ RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235.401
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8767
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-401-2

Query Match 100.0%; Score 61; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQQQFFGLM 11
Db 1 RRPQQQFFGLM 11

RESULT 10
US-08-259-266-2
Sequence 2, Application US/08259266
GENERAL INFORMATION:
APPLICANT: Hipskind, Philip A.
TITLE OF INVENTION: CYCLOHEXYL TACHYKININ RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,266
FILING DATE:

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9335
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-259-266-2

Query Match 100.0%; Score 61; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQQQFFGLM 11
Db 1 RRPQQQFFGLM 11

RESULT 11
US-08-307-741-2
Sequence 2, Application US/08307741
GENERAL INFORMATION:
APPLICANT: Ensing, Geert J
APPLICANT: Panek, Karel J
APPLICANT: Doedens, Barend J
TITLE OF INVENTION: Method of intraoperatively detecting and

TITLE OF INVENTION: Locating tumoural tissues
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wallinckrodt Medical Inc.
STREET: 675 McDonnell Blvd PO box 5840
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,741
FILING DATE: 13-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92200848.7
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: McBride, Thomas P
REGISTRATION NUMBER: 32706
REFERENCE/DOCKET NUMBER: 760US/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-895-2414
TELEFAX: 314-895-2156
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-307-741-2

Query Match 100.0%; Score 61; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQQQFFGLM 11
Db 1 RRPQQQFFGLM 11

RESULT 12
US-08-343-750-2
Sequence 2, Application US/08343750
GENERAL INFORMATION:
APPLICANT: Hipskind, Philip A.
TITLE OF INVENTION: PIPERIDINYL TACHYKININ RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,750
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9789
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-343-750-2

Query Match 100.0%; Score 61; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
|||||

Db 1 RPKPQQFFGLM 11

RESULT 13
US-08-387-056-2
Sequence 2, Application US/08387056
GENERAL INFORMATION:
APPLICANT: Johnson, Kirk W.
TITLE OF INVENTION: METHODS OF TREATING OR PREVENTING
TITLE OF INVENTION: PSYCHIATRIC DISORDERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,056
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9875
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-387-056-2

Query Match 100.0%; Score 61; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
|||||

Db 1 RPKPQQFFGLM 11

RESULT 14
US-08-401-394-2
Sequence 2, Application US/08401394
GENERAL INFORMATION:
APPLICANT: HOESS, RONALD H.
APPLICANT: O'BRIEN, JOHN P.
APPLICANT: SALEMME, FRANCIS R.
TITLE OF INVENTION: STRUCTURAL PROTEINS
TITLE OF INVENTION: FROM ARTIFICIAL GENES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5", 1.0 MB
COMPUTER: MAC INTOSH
OPERATING SYSTEM: MAC INTOSH, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,394
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: NOVEMBER 28, 1990
ATTORNEY/AGENT INFORMATION:
NAME: SIEGELL, BARBARA C.
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: CR-8895-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-401-394-2

Query Match 100.0%; Score 61; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
|||||

Db 1 RPKPQQFFGLM 11

RESULT 15
US-08-401-394A-2
Sequence 2, Application US/08401394A
GENERAL INFORMATION:
APPLICANT: HOESS, RONALD H.
APPLICANT: O'BRIEN, JOHN P.
APPLICANT: SALEMME, FRANCIS R.
TITLE OF INVENTION: STRUCTURAL PROTEINS
TITLE OF INVENTION: FROM ARTIFICIAL GENES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET

CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5", 1.0 MB
COMPUTER: MAC INTOSH
OPERATING SYSTEM: MAC INTOSH, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,394A
FILING DATE: AUGUST 6, 1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CR-8895
FILING DATE: NOVEMBER 28, 1990
ATTORNEY/AGENT INFORMATION:
NAME: SIEGELL, BARBARA C.
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: CR-8895-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-401-394A-2

Query Match 100.0%; Score 61; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
|||||
Db 1 RPKPQQOFFGLM 11

Search completed: March 15, 2002, 14:29:47
Job time: 531 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:20:06 ; Search time 34.92 Seconds
(without alignments)
23.995 Million cell updates/sec

Title: US-09-988-792-1

Perfect score: 61

Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	1 SPHO	substance P - hors
2	61	100.0	11	1 A60654	substance P - guin
3	61	100.0	63	2 JC2412	tachykinin gamma c
4	61	100.0	72	2 I62742	tachykinin A gamma
5	61	100.0	72	2 JC5455	preprotachykinin-A
6	61	100.0	97	2 SI2958	tachykinin delta p
7	61	100.0	112	1 SPRTA	substance P alpha
8	61	100.0	115	1 SPBGB	substance P gamma
9	61	100.0	115	2 S47039	tachykinin 1 precu
10	61	100.0	129	1 SPHUB	neurokinin 1 precu
11	61	100.0	130	1 SPRTB	substance beta p
12	61	100.0	130	1 SPBOB	neurokinin 1 precu
13	61	100.0	130	2 S47038	tachykinin 1 precu
14	61	100.0	130	2 I52526	neurokinin 1 precu
15	58	95.1	11	2 JN0023	substance P - chic
16	50	82.0	11	2 S23308	substance P - rain
17	49	80.3	11	2 S23306	substance P - Atla
18	48	78.7	11	2 S33300	probable substance
19	44	72.1	11	2 F60409	substance P-like p
20	44	72.1	11	2 E60409	substance P-like p
21	44	72.1	12	2 S10059	tachykinin - Afric
22	41	67.2	11	2 A61033	ranatachykinin A -
23	41	67.2	3828	2 T13857	trithorax protein
24	38	62.3	205	2 T30016	hypothetical prote
25	38	62.3	257	2 T10586	small nuclear ribo
26	38	62.3	293	2 T04951	hypothetical prote
27	37	60.7	11	2 C60409	kassinin-like pept
28	37	60.7	11	2 S07203	uperolein - frog (
29	37	60.7	249	2 G75189	hypothetical prote

30 36 59.0 11 2 D60409 kassinin-like pept
31 36 59.0 11 2 B60409 kassinin-like pept
32 36 59.0 12 2 S07436 tachykinin - Afric
33 36 59.0 12 2 S07206 kassinin - Senegal
34 36 59.0 321 2 A64173 conserved hypothet
35 36 59.0 373 2 T02976 probable DNA bindi
36 36 59.0 629 2 T19563 hypothetical prote
37 36 59.0 728 2 E69486 translation elonga
38 35 57.4 133 2 A25777 T-cell receptor be
39 35 57.4 206 2 T33064 hypothetical prote
40 35 57.4 297 2 A83049 hypothetical prote
41 35 57.4 347 2 T05737 probable hordein C
42 35 57.4 474 2 T15511 hypothetical prote
43 35 57.4 494 2 E86671 lysine--trNA ligas
44 35 57.4 512 2 A82296 lysyl--trNA syntet
45 35 57.4 832 2 S76815 hypothetical prote

ALIGNMENTS

RESULT 1

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdardarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 100.0%; Score 61; DB 1; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

DB 1 RPKPQQFFGLM 11

RESULT 2

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685

A;Accession: A60654

A;Molecule type: protein

A;Residues: 1-11 <MUR>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 100.0%; Score 61; DB 1; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11

DB 1 RPKPQQFFGLM 11

```
RESULT 3
JC2412
tachykinin gamma chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: JC2412
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the rat
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2412
A:Molecule type: mRNA
A:Residues: 1-63 <KHA>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:12-21/Product: substance P #status predicted <SUP>
F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly)

Query Match 100.0%; Score 61; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
Db 11 RPKPQQOFFGLM 21

RESULT 4
162742
tachykinin A gamma chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: 162742; JC5453
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287
A:Accession: 162742
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-72 <RES>
A:Cross-references: GB:M68909; NID:9200469; PIDN:AAA39970.1; PID:g554261
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is involved in
C:Genetics:
A:Gene: gamma-PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 100.0%; Score 61; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
Db 23 RPKPQQOFFGLM 33

RESULT 5
JC5455
preprotachykinin-A gamma precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
C:Accession: JC5455; I45967
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287
A:Accession: B26590
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-72 <CHI>
A:Cross-references: GB:M68912; NID:9163593; PIDN:AAA30725.1; PID:g552336
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 100.0%; Score 61; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
Db 23 RPKPQQOFFGLM 33

RESULT 6
SI2958
tachykinin delta precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: SI2958; JC2413
R:Harman, A.J.; Hyde, V.; Chapman, K.
FEBS Lett. 275, 22-24, 1990
A:Title: Identification and cDNA sequence of delta-preprotachykinin, a fourth splicing
A:Reference number: SI2958; MUID:91085565
A:Accession: SI2958
A:Molecule type: mRNA
A:Residues: 1-97 <HAR>
A:Cross-references: GB:X56306; NID:956067; PIDN:CAA39752.1; PID:g56068
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2413
A:Molecule type: mRNA
A:Residues: 48-92 <KHA>
A:Cross-references: GB:S72369; NID:9632805; PIDN:AAB31499.1; PID:g632806
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:59-68/Product: substance P #status predicted <SUP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 100.0%; Score 61; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGLM 11
Db 58 RPKPQQOFFGLM 68

RESULT 7
SPRTA
substance P alpha precursor - rat
N:Alternate names: preprotachykinin alpha
N:Contains: substance P
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: B26590
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and ne
A:Reference number: A94187; MUID:87118268
A:Accession: B26590
```

A:Molecule type: mRNA
A:Residues: 1-112 <KRA>
A:Cross-references: GB:M34184; NID:g206329; PIDN:AAA41925.1; PID:g206330
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the alpha f
C:Comment: The alpha form is processed to yield substance P.
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykin
F:1-12/Product: substance P alpha precursor #status predicted <PREA>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 61; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 58 RPKPQQFFGLM 68

RESULT 8
SPRG
substance P gamma precursor - rabbit
N:Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykinin
N:Contains: neurokinin A; neuropeptide K; substance P
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: JN0709; A60302; A60200; S18922
R:Maegret, H.J.; Heitland, A.; Rose, M.; Forssmann, W.G.
Biochem. Biophys. Res. Commun. 195, 128-131, 1993
A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.
A:Reference number: JN0709; MUID:93371392
A:Accession: JN0709
A:Molecule type: mRNA
A:Residues: 1-115 <MA2>
A:Cross-references: EMBL:X62994; NID:g1565; PIDN:CAA44728.1; PID:g1566
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
Regul. Pept. 18, 346, 1987
A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived from g
A:Reference number: A60302
A:Accession: A60302
A:Molecule type: protein
A:Residues: 72-92 <KAG>
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
J. Neurochem. 50, 1412-1417, 1988
A:Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived fr
A:Reference number: A60200; MUID:88199570
A:Accession: A60200
A:Molecule type: protein
A:Residues: 72-92 <KA2>
C:Comment: The gamma alternatively spliced form is processed to yield substance P and ne
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:72-92/Product: gamma-neuropeptide K #status experimental <NPX>
F:83-92/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
F:92/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 61; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 58 RPKPQQFFGLM 68

RESULT 9
substance P gamma precursor - rabbit
N:Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykinin
N:Contains: neurokinin A; neuropeptide K; substance P
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: JN0709; A60302; A60200; S18922
R:Maegret, H.J.; Heitland, A.; Rose, M.; Forssmann, W.G.
Biochem. Biophys. Res. Commun. 195, 128-131, 1993
A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.
A:Reference number: JN0709; MUID:93371392
A:Accession: JN0709
A:Molecule type: mRNA
A:Residues: 1-115 <MA2>
A:Cross-references: EMBL:X62994; NID:g1565; PIDN:CAA44728.1; PID:g1566
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
Regul. Pept. 18, 346, 1987
A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived from g
A:Reference number: A60302
A:Accession: A60302
A:Molecule type: protein
A:Residues: 72-92 <KAG>
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
J. Neurochem. 50, 1412-1417, 1988
A:Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived fr
A:Reference number: A60200; MUID:88199570
A:Accession: A60200
A:Molecule type: protein
A:Residues: 72-92 <KA2>
C:Comment: The gamma alternatively spliced form is processed to yield substance P and ne
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:72-92/Product: gamma-neuropeptide K #status experimental <NPX>
F:83-92/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
F:92/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 61; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 58 RPKPQQFFGLM 68

RESULT 9
substance P gamma precursor - rabbit
N:Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykinin
N:Contains: neurokinin A; neuropeptide K; substance P
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: JN0709; A60302; A60200; S18922
R:Maegret, H.J.; Heitland, A.; Rose, M.; Forssmann, W.G.
Biochem. Biophys. Res. Commun. 195, 128-131, 1993
A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.
A:Reference number: JN0709; MUID:93371392
A:Accession: JN0709
A:Molecule type: mRNA
A:Residues: 1-115 <MA2>
A:Cross-references: EMBL:X62994; NID:g1565; PIDN:CAA44728.1; PID:g1566
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
Regul. Pept. 18, 346, 1987
A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived from g
A:Reference number: A60302
A:Accession: A60302
A:Molecule type: protein
A:Residues: 72-92 <KAG>
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
J. Neurochem. 50, 1412-1417, 1988
A:Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived fr
A:Reference number: A60200; MUID:88199570
A:Accession: A60200
A:Molecule type: protein
A:Residues: 72-92 <KA2>
C:Comment: The gamma alternatively spliced form is processed to yield substance P and ne
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:72-92/Product: gamma-neuropeptide K #status experimental <NPX>
F:83-92/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
F:92/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

S47039
tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47039
R:Heitland, A.; Kruhoffer, M.; Juergen Maegert, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47039
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <HEI>
A:Cross-references: EMBL:X80663; NID:g520938; PIDN:CAA56692.1; PID:g520939
C:Superfamily: substance P precursor

Query Match 100.0%; Score 61; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||
Db 58 RPKPQQFFGLM 68

RESULT 10
SPHUB
neurokinin 1 precursor, beta splice form [validated] - human
N:Alternate names: neurokinin A; neurokinin alpha; neurokinin L; neuropeptide K; prep
N:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 pre
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1988 #sequence_revision 26-May-1995 #text_change 19-May-2000
C:Accession: A24805; A60425; S00069; S03033; JC5451; JC5450; A59269; A59270; B59270;
R:Harmar, A.J.; Armstrong, A.; Pascall, J.C.; Chapman, K.; Rosie, R.; Curtis, A.; Go
FEBS Lett. 208, 67-72, 1986
A:Title: cDNA sequence of human beta-preprotachykinin, the common precursor to substa
A:Reference number: A24805; MUID:87030957
A:Accession: A24805
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: GB:M28109; EMBL:X54469; NID:g29482; PIDN:CAA38351.1; PID:g29483
R:McGregor, G.P.; Conlon, J.M.
Peptides 11, 907-910, 1990
A:Title: Characterization of the C-terminal flanking peptide of human beta-preprotach
A:Reference number: A60425; MUID:91133994
A:Accession: A60425
A:Molecule type: protein
A:Residues: 111-126 <MCG>
A:Experimental source: neuroendocrine tumor of adrenal medulla
R:Theodorsson-Norheim, E.; Joernvall, H.; Andersson, M.; Norheim, I.; Oeberg, K.; Jac
Eur. J. Biochem. 166, 693-697, 1987
A:Title: Isolation and characterization of neurokinin A, neurokinin A(3-10) and neuro
A:Reference number: S00069; MUID:87275962
A:Accession: S00069
A:Molecule type: protein
A:Residues: 98-107 <THE>
R:Kage, R.; Thim, L.; Creutzfeldt, W.; Conlon, J.M.
Biochem. J. 253, 203-207, 1988
A:Title: Post-translational processing of preprotachykinins. Isolation of protachykin
A:Reference number: S03033; MUID:88339887
A:Accession: S03033
A:Molecule type: protein
A:Residues: 20-30 <KAG>
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5451
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 36-73,89-122 <CHII>
A:Cross-references: GB:M68907; NID:g190292; PIDN:AAA60160.1; PID:g553619
A:Accession: JC5450

A: Status: translation not shown
A: Molecule type: mRNA
A: Residues: 36-86, 'P', 88-122 <CHI2>
A: Cross-references: GB:M68906; NID:g190290; PIDN:AAA60159.1; PID:g553618
R: Tan, A.; Too, H. P.
submitted to GenBank, October 1995
A: Reference number: A59269
A: Accession: A59269
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 1-129 <TAN>
A: Cross-references: GB:U37529; NID:g1017792; PIDN:AAA79195.1; PID:g1017793
A: Experimental source: tissue brain cortex
R: Lai, J. P.; Douglas, S. D.; Rappaport, E.; Wu, J. M.; Ho, W. Z.
submitted to GenBank, February 1998
A: Description: Identification of a delta isoform of preprotachykinin mRNA in human monocytes
A: Reference number: A59270
A: Accession: A59270
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 36-96, 'M', 116-118 <LAI1>
A: Cross-references: GB:AF050656; NID:g3098594; PIDN:AAC15702.1; PID:g3098595
A: Experimental source: alpha splice form; tissue blood; tissue brain; cell type monocytes
A: Accession: B59270
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 36-73, 89-96, 'M', 116-122 <LAI2>
A: Cross-references: GB:AF050659; NID:g3098598; PIDN:AAC15704.1; PID:g3098599
A: Experimental source: delta splice form; tissue blood; tissue brain; cell type monocytes
C: Comment: This protein is processed to produce the tachykinin peptide hormones neurokinin
C: Genetics:
A: Gene: GDB: TAC1; TAC2; NKNA; PPT-A
A: Cross-references: GDB: 119452; OMIM: 162320
A: Map position: 7q21-q22
C: Superfamily: substance P precursor
C: Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F: 1-129/Product: neurokinin 1 precursor, beta splice form #status predicted <SP>
F: 1-96, 'M', 116-118/Product: neurokinin 1 precursor, alpha splice form #status predicted
F: 1-73, 89-129/Product: neurokinin 1 precursor, gamma splice form #status predicted <SP>
F: 1-73, 89-96, 'M', 116-122/Product: neurokinin 1 precursor, alpha splice form #status predicted
F: 1-19/Domain: signal sequence #status predicted <SIG>
F: 20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F: 58-68/Product: neurokinin 1 #status experimental <NK1>
F: 72-107/Product: neuropeptide K #status predicted <NEK>
F: 98-107/Product: neurokinin 2 #status experimental <NK2>
F: 100-107/Product: neurokinin 2 (3-10) #status experimental <NK23>
F: 101-107/Product: neurokinin 2 (4-10) #status experimental <NK24>
F: 111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
F: 68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycosylation)
F: 107/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycosylation)

Query Match	100.0%	Score 61;	DB 1;	Length 129;
Best Local Similarity	100.0%	Pred. No. 0.00049;		
Matches 11;	Conservative	0;	Mismatches 0;	Gaps 0;
			Indels	

Qy 1 RPKPQQFFGLM 11
+ + + + + + + + + +
Db 58 RPKPQQFFGLM 68

RESULT 11

substance P beta precursor - rat
SPRTB
N:Alternate names: preprotachykinin beta; preprotachykinin gamma; substance K
N:Contains: neurokinin A; substance P; substance P gamma precursor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: A37163; A26590; C26590; A25067; JC2411
R:Garter, M.S.; Krause, J.E.
J. Neurosci. 10, 2203-2214, 1990
A:title: Structure, expression, and some regulatory mechanisms of the rat preprotachykinin

A:Reference number: A37163; MUID:90331040
A:Accession: A37163
A:Molecule type: DNA
A:Residues: 1-130 <CAR>
A:Cross-references: GB:M34160; GB:M34160; GB:M34162; NID:g206334; PIDN:AAA41926.1; PI:
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and ne
A:Reference number: A94187; MUID:87118268
A:Accession: A26590
A:Molecule type: mRNA
A:Residues: 1-130 <KRA>
A:Cross-references: GB:M15191; NID:g206341; PIDN:AAA41928.1; PID:g206342; GB:M35277
A:Accession: C26590
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KR2>
A:Cross-references: GB:M34163; NID:g206343; PIDN:AAA41929.1; PID:g206344
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of
A:Reference number: A25067; MUID:87025808
A:Accession: A25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
A:Cross-references: GB:M14312; NID:g206339; PIDN:AAA41927.1; PID:g206340
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2411
A:Molecule type: mRNA
A:Residues: 48-110 <KHA>
A:Experimental source: Intestine
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the beta
C:Comment: The beta and gamma forms are processed to yield substance P and neurokinin
C:Genetics:
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachy
F:1-130/Product: substance P beta precursor #status predicted <PREG>
F:1-73, 89-130/Product: substance P gamma precursor #status predicted <PREG>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <S9P>
F:98-107/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match	100.0%	Score 61	DB 1	Length 130
Best Local Similarity	100.0%	Pred. No. 0.0005		
Matches 11	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 1 RPKPQQFFGLM 11
 Db 58 RPKPQQFFGLM 68

RESULT 12

SPBOB

neurokinin 1 precursor,
N;Alternate names: neuro
N;Contains: neurokinin 1

C;Dale: 13
C;Accessio

R; Nawa, H.; Kotani, H.;

Nature 312, 729-734, 1988.

A;Title: Tissue-specific

A;Reference number: A050

A;Accession: A05093

A;Molecule type: DNA

A;Residues: 1-130 <NAWI>

A;Cross-references: GB:X

R;Nawa, H.; Hirose, T.; Takashima, H.; Inayama, S.; Nakanishi, S.
Nature 306, 32-36, 1983
A;Title: Nucleotide sequences of cloned cDNAs for two types of bovine brain substance P
A;Reference number: A93318; MUID:84039802
A;Accession: A01559
A;Molecule type: mRNA
A;Residues: 1-130 <NAW2>
A;Cross-references: GB:X00075; NID:g758; PIDN:CAA24939.1; PID:g759
A;Accession: A01557
A;Molecule type: mRNA
A;Residues: 1-96, 'M', 116-130 <NAW3>
A;Cross-references: GB:X00076; NID:g762; PIDN:CAA24942.1; PID:g763
R;Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A;Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of a
A;Reference number: A25067; MUID:87025808
A;Accession: B25067
A;Molecule type: mRNA
A;Residues: 1-73, 89-130 <KAW>
R;McGregor, G.P.; Kage, R.; Thim, L.; Conlon, J.M.
J. Neurochem. 53, 1871-1877, 1989
A;Title: Quantitation and characterization of peptides from the C-terminal flanking region
A;Reference number: A61460; MUID:90039314
A;Accession: A61460
A;Molecule type: protein
A;Residues: 111-126 <MCG>
A;Experimental source: Corpus striatum
R;Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A;Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A;Reference number: JC5450; MUID:91209287
A;Accession: JC5454
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 36-120, 'A', 122 <CHI>
A;Cross-references: GB:M68911; NID:g163591; PIDN:AAA30724.1; PID:g52335
C;Comment: The protein is processed to produce neurokinin 1 (substance P) and neurokinin
C;Genetics:
A;Gene: PPT-A
A;Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C;Superfamily: substance P precursor
C;Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F;1-130/Product: neurokinin 1 precursor, beta splice form #status predicted <SPB>
F;1-96, 'M', 116-130/Product: neurokinin 1 precursor, alpha splice form #status predicted
F;1-73, 89-130/Product: neurokinin 1 precursor, gamma splice form #status predicted <SPG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F;58-68/Product: neurokinin 1 #status experimental <SBP>
F;98-107/Product: neurokinin 2 #status predicted <NEK>
F;111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
F;68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
F;107/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 61; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 58 RPKPQQFFGLM 68

RESULT 13
S47038
tachykinin 1 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
A;Accession: S47038
R;Heitland, A.; Kruhoffer, M.; Juergen Maegert, H.J.; Forssmann, W.G.
submitted to the EMBL data Library, July 1994
A;Reference number: S47038
A;Accession: S47038

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <HEI>
A;Cross-references: EMBL:X80662; NID:g520917; PIDN:CAA56691.1; PID:g520918
C;Superfamily: substance P precursor

Query Match 100.0%; Score 61; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 58 RPKPQQFFGLM 68

RESULT 14
I52526
neurokinin 1 precursor - mouse
N;Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N;Contains: neurokinin 1; neurokinin 2
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000
C;Accession: I52526; JC5452; I62741
R;Kako, K.; Munekata, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A;Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and
A;Reference number: I52526
A;Accession: I52526
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-130 <KAK>
A;Cross-references: GB:D17584; NID:g407345; PIDN:BAA04508.1; PID:g435121
R;Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A;Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A;Reference number: JC5450; MUID:91209287
A;Accession: JC5452
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 36-122 <CHI>
A;Cross-references: GB:M68908; NID:g200467; PIDN:AAA39969.1; PID:g554260
C;Genetics:
A;Gene: PPT-A
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F;58-68/Product: neurokinin 1 #status predicted <NK1>
F;98-107/Product: neurokinin 2 #status predicted <NK2>
F;111-126/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F;107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 100.0%; Score 61; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | |
Db 58 RPKPQQFFGLM 68

RESULT 15
JN0023
substance P - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
A;Accession: JN0023
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A:Reference number: JN0023; MUID:88204263
A:Accession: JN0023
A:Molecule type: protein
A:Residues: 1-11 <CON>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 95.1%; Score 58; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00015;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPRPQQFFGLM 11
DB 1 RPRPQQFFGLM 11

Search completed: March 15, 2002, 14:23:47
Job time: 221 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:22:31 ; Search time 48.07 Seconds
(without alignments)
14.595 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 302707 seqs, 63781257 residues

Total number of hits satisfying chosen parameters: 302707

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep1.*
7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	6	US-09-988-792-1
2	61	100.0	11	6	US-09-988-792-7
3	61	100.0	11	6	US-09-570-022-1
4	61	100.0	11	7	US-10-002-593-4
5	61	100.0	11	7	US-10-053-669-3
6	61	100.0	12	6	US-09-489-667B-2
7	61	100.0	12	6	US-09-489-667B-5
8	61	100.0	12	6	US-09-489-667B-8
9	61	100.0	12	7	US-10-050-200-55
10	61	100.0	13	6	US-09-489-667B-3
11	61	100.0	13	6	US-09-489-667B-6
12	61	100.0	13	6	US-09-489-667B-9
13	61	100.0	14	6	US-09-489-667B-4
14	61	100.0	14	6	US-09-489-667B-7
15	61	100.0	14	6	US-09-489-667B-10
16	61	100.0	20	6	US-09-570-022-23
17	58	95.1	11	6	US-09-988-792-8
18	56	91.8	11	6	US-09-489-667B-1
19	56	91.8	11	6	US-09-988-792-13
20	56	91.8	11	6	US-09-935-682-64
21	53	86.9	11	6	US-09-570-022-5
22	52	85.2	9	6	US-09-489-667B-13
23	51	83.6	9	7	US-10-001-945-18
24	50	82.0	11	6	US-09-988-792-10
25	49	80.3	11	6	US-09-988-792-9

ALIGNMENTS

RESULT 1
US-09-988-792-1
; Sequence 1, Application US/09988792
; GENERAL INFORMATION:
; APPLICANT: Lipkowski, Andrezej W
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: 18475-025
; CURRENT APPLICATION NUMBER: US/09/988,792
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,369
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-988-792-1

Query Match 100.0%; Score 61; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 2
US-09-988-792-7
; Sequence 7, Application US/09988792
; GENERAL INFORMATION:
; APPLICANT: Lipkowski, Andrezej W
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: 18475-025
; CURRENT APPLICATION NUMBER: US/09/988,792
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,369
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Cavia porcellus

Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 70, Appli
Sequence 50, Appli
Sequence 12, Appli
Sequence 15, Appli
Sequence 17, Appli
Sequence 5812, Ap
Sequence 5811, Ap
Sequence 53206, A
Sequence 78408, A
Sequence 5810, Ap
Sequence 53204, A
Sequence 78406, A
Sequence 11326, A
Sequence 11325, A
Sequence 32046, A
Sequence 35428, A
Sequence 35427, A

US-09-988-792-7

Query Match 100.0%; Score 61; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | | |
Db 1 RPKPQQFFGLM 11

RESULT 3

US-09-570-022-1
; Sequence 1, Application US/09570022
; GENERAL INFORMATION:
; APPLICANT: GORDON, RICHARD K.
; APPLICANT: MOORAD, DEBORAH R.
; APPLICANT: DOCTOR, BHUPENDRA P.
; APPLICANT: GARCIA, GREGORY E.
; TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
; FILE REFERENCE: 38644-170531
; CURRENT APPLICATION NUMBER: US/09/570,022
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: 60/134,446
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-570-022-1

Query Match 100.0%; Score 61; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | | |
Db 1 RPKPQQFFGLM 11

RESULT 4

US-10-002-593-4
; Sequence 4, Application US/10002593
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Brown, Nancy J.
; TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTIN
; FILE REFERENCE: ATY Docket No. 1242/48/2
; CURRENT APPLICATION NUMBER: US/10/002,593
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/244,524
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-593-4

Query Match 100.0%; Score 61; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | | |

Db 1 RPKPQQFFGLM 11

RESULT 5

US-10-053-669-3
; Sequence 3, Application US/10053669
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDATION
US-10-053-669-3

Query Match 100.0%; Score 61; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | | |
Db 1 RPKPQQFFGLM 11

RESULT 6

US-09-489-667B-2
; Sequence 2, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Precursor to substance P, wh
; OTHER INFORMATION: is very well known in the art.
US-09-489-667B-2

Query Match 100.0%; Score 61; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
| | | | | | | | | | | |
Db 1 RPKPQQFFGLM 11

RESULT 7

US-09-489-667B-5
; Sequence 5, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain

; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester syn
; OTHER INFORMATION: hetic precursor to substance P.
; NAME/KEY: MISC_FEATURE
; LOCATION: (12)..(12)
; OTHER INFORMATION: Xaa at position 12 is Glycine Methyl Ester
US-09-489-667B-5

Query Match 100.0%; Score 61; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 8

US-09-489-667B-8
; Sequence 8, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester syn
; OTHER INFORMATION: hetic precursor to substance P.
; NAME/KEY: MISC_FEATURE
; LOCATION: (12)..(12)
; OTHER INFORMATION: Xaa at position 12 is Glycine Ethyl Ester
US-09-489-667B-8

Query Match 100.0%; Score 61; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 9

US-10-050-200-55
; Sequence 55, Application US/10050200
; GENERAL INFORMATION:
; APPLICANT: Fourie, Anne
; APPLICANT: Coles, Fawn
; APPLICANT: Karlsson, Lars
; TITLE OF INVENTION: Aggrrecanase-1 and -2 Peptide Substrates and Methods
; FILE REFERENCE: ORT-1417
; CURRENT APPLICATION NUMBER: US/10/050,200
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 55
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide substrate
US-10-050-200-55

Query Match 100.0%; Score 61; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 2 RPKPQQFFGLM 12

RESULT 10

US-09-489-667B-3
; Sequence 3, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a precursor to subst
; OTHER INFORMATION: e P and is very well known in the art.
US-09-489-667B-3

Query Match 100.0%; Score 61; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 RPKPQQFFGLM 11

RESULT 11

US-09-489-667B-6
; Sequence 6, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester s
; OTHER INFORMATION: hetic precursor to substance P.
; NAME/KEY: MISC_FEATURE
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa at position 13 is Lysine Methyl Ester
US-09-489-667B-6

Query Match 100.0%; Score 61; DB 6; Length 13;

Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||||

Db 1 RPKPQOFFGLM 11

RESULT 12

US-09-489-667B-9

; Sequence 9, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester syn
; NAME/KEY: MISC_FEATURE
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa at position 13 is Lysine Ethyl Ester
US-09-489-667B-9

Query Match 100.0%; Score 61; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||||

Db 1 RPKPQOFFGLM 11

RESULT 13

US-09-489-667B-4

; Sequence 4, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a precursor to substance
; OTHER INFORMATION: e p and is very well known in the art.
US-09-489-667B-4

Query Match 100.0%; Score 61; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||||

Db 1 RPKPQOFFGLM 11

RESULT 14

US-09-489-667B-7

; Sequence 7, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester s
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa at position 14 is Arginine Methyl Ester
US-09-489-667B-7

Query Match 100.0%; Score 61; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||||

Db 1 RPKPQOFFGLM 11

RESULT 15

US-09-489-667B-10

; Sequence 10, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester s
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa at position 14 is Arginine Ethyl Ester
US-09-489-667B-10

Query Match 100.0%; Score 61; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
|||||

Db 1 RPKPQOFFGLM 11

Search completed: March 15, 2002, 14:31:51
Job time: 560 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:16:20 ; Search time 66.25 Seconds
(without alignments)
12.299 Million cell updates/sec

Title: US-09-988-792-1

Perfect score: 61

Sequence: 1 RPKPQQFFGLM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101:*

- 1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SID58/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	7 AAP61480	Sequence of undeca
2	61	100.0	11	9 AAP80312	Sequence of neurop
3	61	100.0	11	12 AAR13162	Sialic acid-bonded
4	61	100.0	11	12 AAR11854	Undecapeptide subs
5	61	100.0	11	13 AAR21938	Substance P [Me-Le
6	61	100.0	11	13 AAR21942	Substance P [MeMet
7	61	100.0	11	13 AAR21946	Substance P [Me-Ph
8	61	100.0	11	13 AAR21954	Substance P [Me-GI
9	61	100.0	11	13 AAR21962	Substance P [Me GI
10	61	100.0	11	13 AAR21963	Substance P [p-Chl
11	61	100.0	11	13 AAR28442	Substance P. Synt

12	61	100.0	11	14 AAR42646	Neurokinin 1 recep
13	61	100.0	11	16 AAR85243	Substance p peptid
14	61	100.0	11	16 AAR77310	Substance p. Synt
15	61	100.0	11	18 AAW33180	Mouo-DTPA-Argi Sub
16	61	100.0	11	18 AAW04616	Substance p peptid
17	61	100.0	11	19 AAW42973	Substrate p report
18	61	100.0	11	20 AAY030985	Non-crosslinked pr
19	61	100.0	11	20 AAY03156	Substance p. Synt
20	61	100.0	11	20 AAW92715	Human tachykinin a
21	61	100.0	11	20 AAW92719	Human tachykinin a
22	61	100.0	11	20 AAW92720	Human tachykinin a
23	61	100.0	11	20 AAW92708	Human tachykinin a
24	61	100.0	11	20 AAW92680	Human tachykinin a
25	61	100.0	11	20 AAW92681	Human tachykinin a
26	61	100.0	11	20 AAW92676	Human tachykinin a
27	61	100.0	11	20 AAW92731	Human tachykinin a
28	61	100.0	11	20 AAW79662	Substance P deriva
29	61	100.0	11	20 AAW79663	Substance P deriva
30	61	100.0	11	21 AAB18483	Peptide substrate
31	61	100.0	11	21 AAB23027	Human/rat tachykin
32	61	100.0	11	21 AAY32382	Cell differentiat
33	61	100.0	11	22 AAG62768	Amino acid sequenc
34	61	100.0	11	22 AAG99354	Substance p peptid
35	61	100.0	11	22 AAB84527	Amino acid sequenc
36	61	100.0	11	22 AAB98866	Chimeric analgesic
37	61	100.0	11	22 AAB82070	Substance p. Unid
38	61	100.0	11	22 AAB91436	Tachykinins peptid
39	61	100.0	11	22 AAB91449	Tachykinins peptid
40	61	100.0	11	22 AAB91450	Tachykinins peptid
41	61	100.0	11	22 AAB50544	Prolyl endopeptida
42	61	100.0	11	22 AAB50306	Substance p. Unid
43	61	100.0	12	14 AAR32798	Tyr-1 substance p
44	61	100.0	12	16 AAR85244	Substance p analog
45	61	100.0	12	22 AAB98873	Chimeric analgesic

ALIGNMENTS

RESULT 1

AAP61480

ID AAP61480 standard; peptide; 11 AA.

XX AC AAP61480;

XX DT 22-AUG-1991 (first entry)

XX DE Sequence of undeca peptide substance P1.

XX KW Hypertension therapy; sleep disorder; anti-stress agent.

XX FH Key Location/Qualifiers

XX FT Misc-difference 11 /label= Met-NH2

XX PN DD229593-A.

XX PD 13-NOV-1985.

XX PF 28-NOV-1984; 84DD-0269954.

XX PR 28-NOV-1984; 84DD-0269954.

XX (DEAK) AKAD WISSENSCHAFT DDR.

XX PI Oehme P, Hecht K, Wachtel E, Roske I, Kolometsewa IA.

XX PI Airapetjan M, Bienert M, Vogt WE, Hilse H, Gores E, Poppei M;

XX PI Nieber K, Bergmann J;

XX XX WPI; 1986-069587/11.

XX DR Cpd. having N-terminal sequences of undeca:peptide substance p -

XX PT are medicinal agents with anti-stress activity

XX
PS
XX
CC
CC
CC
CC
CC
CC
XX
XX
SQ

Claim 1; Page 1; 15pp; German.

The inventors claim an antistress compound which contains the N-terminal SQ of AAP61480, pref. Arg-Pro-Lys-Pro-X (X= COOH or NH2). Compared with the full undecapeptide they have much reduced side effects (acute hypotension, spastic effects on the ileum and histamine release from peritoneal mast cells).

SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
| | | | | | | | | |
Db 1 rpkpqffglm 11

RESULT 2

AAP80312
ID AAP80312 standard; protein; 11 AA.

XX
AC AAP80312;

XX
DT 14-SEP-1990 (first entry)

XX
DE Sequence of neuropeptide substance P which binds with polypeptide receptor for bombesin type polypeptides.

XX
KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW substance P.

XX
OS Swiss 3T3 cells.

XX
FH Key Location/Qualifiers

XX
FT Misc-difference 11

XX
FT /Label=OTHER

XX
FT /note="Met-NH2"

XX
PN WO8807551-A.

XX
PD 06-OCT-1988.

XX
PF 31-MAR-1988; 88WO-GB00255.

XX
PR 25-NOV-1987; 87GB-0027638.

XX
PA (IMCR) IMPERIAL CANCER RES.

XX
PI Rosengurt E, Zachary I, Woll P;

XX
DR WPI; 1988-292842/41.

XX
PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation

XX
PS Disclosure; Table 2; 42pp; English.

XX
CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist B. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7, 9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue

XX
CC
CC
CC
CC
CC
XX
SQ

of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
potent than either A or D. Spantide (B) had no antagonist activity even
at 100 uM. Polypeptide antagonists A and D and novel variants are useful
for diagnosis and therapy, esp. of cancers where uncontrolled cell
growth is associated with disorders of proteins of the bombesin family.

SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
| | | | | | | | | |
Db 1 rpkpqffglm 11

RESULT 3

AAR13162
ID AAR13162 standard; Protein; 11 AA.

XX
AC AAR13162;

XX
DT 10-OCT-1991 (first entry)

XX
DE Sialic acid-bonded polypeptide (2).

XX
KW Sialic acid; cataract; immune disorder.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

XX
FT Modified-site 1

XX
FT /note= "N-terminally glycosylated by 5-acetamido-
2,4,7,8,9-penta-O-acetyl-3,5-deoxy-beta-
D-glycero-D-galactonolopyranosyl"

XX
PN JP03151398-A.

XX
PD 27-JUN-1991.

XX
PF 06-NOV-1989; 89JP-0288560.

XX
PR 06-NOV-1989; 89JP-0288560.

XX
PA (MECT-) MECT KK.

XX
DR WPI; 1991-233839/32.

XX
PT New sialic acid derivs. bonded to physiologically active
PT polypeptide - for treatment of cataracts, immune disorders etc.
PT with prolonged half-life

XX
PS Example 4; Page 6; 7pp; Japanese.

XX
CC The prod. has prolonged half-life and is used as a pharmaceutical
CC for treatment of various diseases, such as cataract and immune
CC disorders. It comprises a peptide, N-terminally glycosylated by
CC (opt. acetylated) sialic acid.
CC See also AAR12932, AAR13162 and AAR13201.

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
| | | | | | | | | |
Db 1 rpkpqffglm 11

FT		/note= "OTHER = Me-Leu"
XX	W09202248-A.	
PN		
XX	20-FEB-1992.	
XX		
PF	29-JUL-1991; 91WO-US05323.	
XX		
PR	27-JUL-1990; 90US-0559173.	
XX	(CHIL-) CHILDRENS MED CENT.	
PA		
XX	Yankner BA;	
PI		
XX	WP1; 1992-079804/10.	
DR		
XX	Treatment of neuronal accumulation of beta-amyloid - using	
PT	tachykinin agonists e.g. substance P, physalaemin and neurokinin	
PT	B, for treating Alzheimer's disease, Downs syndrome, etc.	
XX	Claim 10; Page 21; 35pp; English.	
XX	The peptide is the tachykinin agonist substance P with Me-Leu	
CC	substituted at position 10. The peptide was synthesised	
CC	by standard solid phase synthesis. Neuronal accumulation of	
CC	beta-amyloid may be treated by administration of tachykinin	
CC	agonists. The peptides can reduce the neurotoxic effects of a	
CC	beta-amyloid related polypeptide on cultured neurons. The peptide	
CC	and its analogues are useful for controlling diseases characterised	
CC	by beta amyloid accumulation in the brain such as Alzheimers	
CC	disease and Down's syndrome.	
CC	See also AAR21932-75.	
XX		
XX	Sequence 11 AA;	
SQ		
	Query Match 100.0%; Score 61; DB 13; Length 11;	
	Best Local Similarity 100.0%; Pred. No. 0.00029;	
	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gap	
QY	1 RPKPQQOFFGLM 11	
Db	1 rpkpgqffglm 11	
RESULT 6		
AAR21942	ID AAR21942 standard; Protein; 11 AA.	
XX	AAR21942;	
AC		
XX	25-JUN-1992 (first entry)	
DT		
XX	Substance P [MeMet 11].	
DE		
XX	Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;	
KW	syndrome; hereditary cerebral haemorrhage.	
KW		
XX	Synthetic.	
OS		
XX	Key Location/Qualifiers	
FF	Misc-difference 11	
FT	/label= OTHER	
FT	/note= "OTHER = Methyl Methionine"	
XX		
PN	W09202248-A.	
XX		
PD	20-FEB-1992.	
XX		
PF	29-JUL-1991; 91WO-US05323.	
XX		
PR	27-JUL-1990; 90US-0559173.	
XX		

PA (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

CC The peptide is the tachykinin agonist substance P with a methyl
CC methionine residue substituted at position 11. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00029;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

DB 1 rpkpqffgglm 11

RESULT 7

AAR21946

ID AAR21946 standard; Protein; 11 AA.

XX AAR21946;

DT 25-JUN-1992 (first entry)

XX Substance P [Me-Phe 8].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 8

FT /label= OTHER

FT /note= "OTHER = Methyl phenylalanine"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX

Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a methyl
CC phenylalanine residue substituted at position 8. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00029;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11

DB 1 rpkpqffgglm 11

RESULT 8

AAR21954

ID AAR21954 standard; Protein; 11 AA.

XX AAR21954;

DT 25-JUN-1992 (first entry)

XX Substance P [Me-Gly 9].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 9

FT /label= OTHER

FT /note= "OTHER = Methyl glycine"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 22; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a methyl
CC glycine residue substituted at position 9. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as

CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
 | | | | | | | | | |
 Db 1 rpkpqffgilm 11

RESULT 9

AAR21962
 ID AAR21962 standard; Peptide; 11 AA.

XX AAR21962;

XX 25-JUN-1992 (first entry)

XX Substance P [Me Gly 6, Met (O2) 11].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 6

FT /label= OTHER
 FT /note= "OTHER - Methyl glycine"

FT Misc-difference 11

FT /label= OTHER
 FT /note= "OTHER - Met (O2)"

XX W09202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 22; 35pp; English.

XX The peptide is the tachykinin agonist, substance P with methyl
 CC glycine substituted at position 9 and Met (O2) at position 11.
 CC The peptide was synthesised by standard solid phase synthesis.
 CC Neuronal accumulation of beta-amyloid may be treated by administ-
 CC ration of tachykinin agonists. The peptide can reduce the neuro-
 CC toxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
 | | | | | | | | | |
 Db 1 rpkpqffgilm 11

RESULT 10

AAR21963
 ID AAR21963 standard; Peptide; 11 AA.

XX AAR21963;

XX 25-JUN-1992 (first entry)

XX Substance P [p-Chloro-Phe 7,8].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 7

FT /label= OTHER
 FT /note= "p-Chloro-phenylalanine"

FT Modified-site 8

FT /label= OTHER
 FT /note= "p-Chloro-phenylalanine"

XX W09202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 22; 35pp; English.

XX The peptide is the tachykinin agonist, substance P fragment
 CC with p-Chloro-phenylalanine residues substituted at positions 7 and
 CC 8. The peptide was synthesised by standard solid phase synthesis.
 CC Neuronal accumulation of beta-amyloid may be treated by administ-
 CC ration of tachykinin agonists. The peptide can reduce the neuro-
 CC toxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
 | | | | | | | | | |
 Db 1 rpkpqffgilm 11

```

RESULT 11
AAR28442
ID AAR28442 standard; peptide; 11 AA.
XX
AC AAR28442;
XX
DT 22-MAR-1993 (first entry)
XX
DE Substance P.
XX
KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;
KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
KW granuloma; Crohn's disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "amidated"
XX
PN W09218536-A.
XX
PD 29-OCT-1992.
XX
PF 22-APR-1992; 92WO-US03307.
XX
PR 22-APR-1991; 91EP-0200955.
XX
PA (MLCW ) MALLINCKRODT MEDICAL INC.
XX
PI Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
XX
DR WPI; 1992-382047/46.
XX
PT Detection and localisation of tissues with neurokinine-1 receptors
PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.
XX
PS Disclosure; Page 4; 22pp; English.
XX
CC Substance P or its Tyr0 deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain
CC tissues. See also AAR28443-R28446.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 rpkpqqffglm 11

RESULT 12
AAR42646
ID AAR42646 standard; peptide; 11 AA.
XX
AC AAR42646;
XX
DT 19-APR-1994 (first entry)
XX
DE Neurokinin 1 receptor affinity-contg. peptide (Substance P).
XX
KW Neurokinin 1; somatostatin; receptor; cytokine; growth factor;
KW hormone; intra-operativ; tumour; low energy gamma photon;

Query Match 100.0%; Score 61; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 rpkpqqffglm 11

RESULT 13
AAR85243
ID AAR85243 standard; peptide; 11 AA.
XX
AC AAR85243;
XX
DT 18-AUG-1997 (first entry)
XX
DE Substance P peptide.
XX
KW Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KW Systematic Evolution of Ligands by Exponential enrichment; primer;
KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
KW diabetic retinopathy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "contains C-terminal NH2 group"
XX
PN W09530775-A1.
XX
PD 16-NOV-1995.

```

```

KW radionuclide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "the C-terminal is amidated"
XX
PN W09318797-A.
XX
PD 30-SEP-1993.
XX
PF 24-MAR-1993; 93WO-US02772.
XX
PR 25-MAR-1992; 92EP-0200848.
XX
PA (MLCW ) MALLINCKRODT MEDICAL INC.
XX
PI Doedens BJ, Ensing GJ, Panek KJ;
XX
DR WPI; 1993-320461/40.
XX
PT Intra-operatively detecting and locating tumour tissues - using
PT specific peptide(s) labelled with low energy gamma photon
PT emitting radionuclide
XX
PS Disclosure; Page 4; 31pp; English.
XX
CC The method of intraoperatively detecting and locating tumoral
CC tissues makes use of peptides having selective neurokinin 1
CC receptor affinity (AAR42644; generic formula; AAR42646-R42650;
CC specific examples), peptides having selective somatostatin
CC receptor affinity (AAR42645; generic formula; AAR42651-R42660;
CC specific examples), and peptides selected from cytokines,
CC growth factors and hormones.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 rpkpqqffglm 11

RESULT 13
AAR85243
ID AAR85243 standard; peptide; 11 AA.
XX
AC AAR85243;
XX
DT 18-AUG-1997 (first entry)
XX
DE Substance P peptide.
XX
KW Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KW Systematic Evolution of Ligands by Exponential enrichment; primer;
KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
KW diabetic retinopathy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "contains C-terminal NH2 group"
XX
PN W09530775-A1.
XX
PD 16-NOV-1995.

```

XX PF 03-MAY-1995; 95WO-US05600.
XX PR 21-DEC-1994; 94US-0361795.
XX PR 06-MAY-1994; 94US-0238863.
XX PR 24-MAY-1994; 94US-02488632.
XX PR 09-SEP-1994; 94US-0303362.
XX PR 11-JUN-1990; 90US-0536428.
XX PR 10-JUN-1991; 91US-0714131.
XX PR 21-OCT-1992; 92US-0964624.
XX PA (UYRE-) UNIV RES CORP.
XX PI Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;
XX PI Schneider DJ, Sullenger BA, Wecker M;
XX DR WPI; 1995-404132/51.
XX PT Systematic evolution of ligands by exponential enrichment - for
XX PT identifying nucleic acid ligands used in the treatment of, e.g. type
XX PT B insulin resistance and HIV
XX PS Example 10; Fig 8; 209pp; English.
XX CC The invention relates to a novel method of isolating ligands that bind
XX CC to target proteins e.g. antibodies or receptors, which bind other
XX CC proteins or ligands. The method, designated Systematic Evolution of
XX CC Ligands by Exponential enrichment (SELEX), comprises generating a library
XX CC of random oligonucleotide sequences, about 40-60 nucleotides in length,
XX CC and binding these sequences to the target proteins. After removal of
XX CC unbound material, the remaining bound nucleotide sequences are amplified
XX CC e.g. by PCR, and the newly amplified material is bound again with the
XX CC target protein. This cycle continues until a sufficiently pure
XX CC oligonucleotide sequence is isolated. The method allows the isolation of
XX CC oligonucleotide sequences which structurally mimic the target protein's
XX CC ligand. Ligands AAR06098-130 are examples of nucleic acid ligands which
XX CC bind the tachykinin-family neuropeptide Substance P (this sequence). The
XX CC new ligands were split into 2 groups based on their affinities for
XX CC Substance P. Class 1 ligands had binding affinities up to 2 micromolar
XX CC whereas class 2 ligands bound at above 2 micromolar. This sequence
XX CC represents the consensus of the class 1 ligands. The ligands can be
XX CC used to block the activity of Substance P and is useful in the treatment
XX CC of e.g. rheumatoid arthritis, atherosclerosis, diabetic retinopathy or
XX CC cancer.
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 rpkpqffg1m 11

RESULT 14
AAR77310
ID AAR77310 standard; peptide; 11 AA.
XX AC AAR77310;
XX XX
XX 08-MAR-1996 (first entry)
XX DE Substance P.
XX KW Substance P; neurokinin; neurokinin receptor antagonist;
XX KW sensory perception; tachykinin receptor; therapy;
XX KW neurodegenerative disorder; Alzheimer's disease; demyelinating disease;
XX KW multiple sclerosis; respiratory disease; ophthalmic disease;
XX KW addition disorder; adverse immune reaction; gastrointestinal disorder;
XX KW bladder function disorder; fibrosing disease; collagen disease;

KW diagnosis.
XX XX
XX Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 11
XX FT /note= "amidated"
XX PN US5434158-A.
XX PD 18-JUL-1995.
XX XX
XX PF 26-APR-1994; 94US-0233487.
XX PR 26-APR-1994; 94US-0233487.
XX XX (WERI) MERCK & CO INC.
XX PA Shah SK;
XX PI WPI; 1995-268290/35.
XX DR
XX PT New 1'-substd. spiro-indoline-3,4'-piperidine derivs. - useful as
XX PT selective neurokinin-3 antagonists, e.g. for treating CNS disorders,
XX PT migraine or esp. asthma.
XX PS Disclosure; Column 1; 16pp; English.
XX CC This sequence represents Substance P. This sequence, and those shown in
XX CC AAR77311 and AAR77312 are tachykinins. These three sequences are
XX CC pharmacologically active neuropeptides, and are neurokinin receptor
XX CC agonists. Neurokinin receptors are widely distributed throughout the
XX CC mammalian nervous system, circulatory system and peripheral tissues.
XX CC Neurokinin receptors are involved in sensory perception. These
XX CC sequences were used in the design and testing of neurokinin antagonists.
XX CC These antagonists could be used in the treatment of conditions
XX CC characterised by overstimulation of tachykinin receptors. The
XX CC antagonists can also be used, for the treatment of neurodegenerative
XX CC disorders (e.g. Alzheimer's disease), demyelinating diseases (e.g.
XX CC multiple sclerosis), respiratory diseases, ophthalmic diseases, addition
XX CC disorders, adverse immune reactions, gastrointestinal disorders, bladder
XX CC function disorders, fibrosing and collagen diseases. The antagonists can
XX CC also be used as diagnostic agents.
XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
Db 1 rpkpqffg1m 11

RESULT 15
AAW33180
ID AAW33180 standard; peptide; 11 AA.
XX AC AAW33180;
XX XX
XX 29-JAN-1998 (first entry)
XX DE Mono-DTPA-Arg1 Substance P.
XX KW Substance P; radiolabel; diagnostic imaging; therapy;
XX KW mono-DTPA-Arg1.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1

FT	/note=	"DTPA-Arg"
FT	Modified-site	11
FT	/note=	"amidated"

WO9640292-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US09706.

07-JUN-1995; 95US-0480372.

(MLCW) MALLINCKRODT MEDICAL INC.

Srinivasan A:

WPI; 1997-087027/08.

Prepn. of pure radio:labelled peptide, e.g. for diagnostic imaging -
 PT by combining protected poly(amino:carboxylate) ligand with peptide
 PT and forming complex with radionuclide

Example 3; Page 12; 20pp; English.

Preparing a radiolabelled peptide composition, comprises combining a triamine or diamine chelating agent with a peptide, e.g. the present peptide, in a solid phase peptide synthesiser, and complexing a radionuclide with the chelate-peptide conjugate. Radiolabelled peptides or peptidomimetics can be used as diagnostic imaging agents, or in therapeutic applications, e.g. iodine(111) labelled pentacotide can be used for somatostatin receptor imaging of neuroendocrine tumours. The radiolabelled products are obtained efficiently and inexpensively in high purity. The protected polyaminocarboxylate ligands can be added to the peptide by standard solution or solid phase peptide synthesis and deprotected with conventional reagents to give only the mono-addition product, free of di-addition product impurities. The deprotected product can be labelled with medically useful radionuclides, e.g. lanthanides or actinides, at any desired location. Pre-derivatisation of individual amino acids is not required.

Sequence 11 AA:

```

Query Match      100.0%; Score 61; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 RPKPQQFFGLM 11

Db 1 rpkpqafqalm 11

Search completed: March 15, 2002, 14:22:27
Job time: 367 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:30:59 ; Search time 63.84 seconds
(without alignments)
25.204 Million cell updates/sec

Title: US-09-988-792-13
Perfect score: 57
Sequence: 1 RPKPQQFFGLX 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTEMBL_17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	56	98.2	72	4 Q9Y494	Q9Y494 homo sapien
2	56	98.2	114	6 Q97947	Q97947 tupaia bela
3	56	98.2	128	4 Q9Y6V5	Q9Y6V5 homo sapien
4	56	98.2	129	6 Q97948	Q97948 tupaia bela
5	48	84.2	97	11 Q9Z0K2	Q9Z0K2 cavia porce
6	48	84.2	115	11 Q9Z0K1	Q9Z0K1 cavia porce
7	48	84.2	130	11 Q9Z0K0	Q9Z0K0 cavia porce
8	39	68.4	786	5 Q24014	Q24014 dictyosteli
9	39	68.4	803	5 Q24012	Q24012 dictyosteli
10	38	66.7	205	5 Q20174	Q20174 caenorhabdi
11	38	66.7	207	1 Q9HLY7	Q9HLY7 thermoplasm
12	38	66.7	235	5 Q9BWA4	Q9BWA4 drosophila
13	38	66.7	257	1 Q9SUN5	Q9SUN5 arabidopsis
14	37	64.9	249	1 Q9V2N2	Q9V2N2 pyrococcus
15	37	64.9	3722	2 P94873	P94873 lysobacter
16	36	63.2	177	5 Q9BPN9	Q9BPN9 caenorhabdi
17	36	63.2	236	5 Q9NEW8	Q9NEW8 caenorhabdi
18	36	63.2	352	12 Q86283	Q86283 unidentified
19	36	63.2	477	3 Q9UW05	Q9UW05 clavispore

20	36	63.2	550	5 Q94130	Q94130 caenorhabdi
21	36	63.2	629	5 Q45273	Q45273 caenorhabdi
22	36	63.2	869	2 Q9F634	Q9F634 stigmatella
23	35	61.4	138	2 Q84949	Q84949 salmonella
24	35	61.4	206	5 Q61761	Q61761 caenorhabdi
25	35	61.4	296	10 Q9LVZ6	Q9LVZ6 arabidopsis
26	35	61.4	347	10 Q40055	Q40055 hordeum vul
27	35	61.4	373	10 Q23876	Q23876 oryza sativ
28	35	61.4	494	2 Q9CII7	Q9CII7 lactococcus
29	35	61.4	497	2 Q9A0V7	Q9A0V7 streptococc
30	35	61.4	509	12 Q65191	Q65191 african swi
31	35	61.4	521	5 Q18014	Q18014 caenorhabdi
32	35	61.4	681	5 Q9GUT4	Q9GUT4 leishmania
33	35	61.4	682	11 Q9ESL2	Q9ESL2 cavia porce
34	35	61.4	832	2 P74619	P74619 synchocyst
35	34	5	216	10 Q9CAM3	Q9CAM3 arabidopsis
36	34	59.6	154	11 Q9JK11	Q9JK11 mus pahari
37	34	59.6	167	2 Q9X8G5	Q9X8G5 streptomyce
38	34	59.6	266	12 Q56868	Q56868 gallid herp
39	34	59.6	270	5 Q9UGU0	Q9UGU0 caenorhabdi
40	34	59.6	306	2 Q9JXY6	Q9JXY6 neisseria m
41	34	59.6	316	5 Q76902	Q76902 drosophila
42	34	59.6	318	2 Q9JYV5	Q9JYV5 neisseria m
43	34	59.6	355	8 Q9MJ81	Q9MJ81 physarum po
44	34	59.6	359	10 Q82469	Q82469 mesembryant
45	34	59.6	393	10 Q49132	Q49132 diospyros k

ALIGNMENTS

RESULT 1					
Q9Y494					
ID Q9Y494	PRELIMINARY;	PRT;	72 AA.		
AC Q9Y494;					
DT 01-NOV-1999 (TEMBLrel. 12, Created)					
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)					
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)					
DE GAMMA PREPROTACHYKININ (FRAGMENT).					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=BLOOD, AND BRAIN;					
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;					
RT "Identification of a Delta Isoform of preprotachykinin mRNA in Human					
RT Mononuclear Phagocytes and Lymphocytes."					
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AF050657; AAC15703.1; -					
DR InterPro: IPR002040; Tachykinin.					
DR InterPro: IPR003580; Protachykinin.					
DR Pfam; PF02202; Tachykinin; 1.					
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.					
DR SMART; SM00203; TK; 2.					
FT NON_TER 1					
FT NON_TER 72					
SQ SEQUENCE 72 AA; 8274 MW; 2C02B2BA41EAAD16 CRC64;					

Query Match 98.2%; Score 56; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
| | | | | | | | | |
Db 23 RPKPQQFFGL 32

RESULT 2
Q97947 PRELIMINARY; PRT; 114 AA.
ID Q97947

```

AC O97947;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ I.
OS Tupala belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50785; CAA90648.1; -.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 83 92 NEUROKININ A.
SQ SEQUENCE 114 AA; 13281 MW; B439C3D27FD47CAB CRC64;

Query Match 98.2%; Score 56; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGL 10
| | | | | | | | | |
Db 58 RPKPOQFFGL 67

RESULT 3
O9Y6V5 PRELIMINARY; PRT; 128 AA.
AC O9Y6V5;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE WUGSC:H-DJ0841B21.1 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalicki J., Angell S.;
RT "The sequence of Homo sapiens PAC clone DJ0841B21.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004140; AAC02754.1; -.
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 1.
SQ SEQUENCE 128 AA; 14770 MW; 0F8D61774AFEC1CA CRC64;

Query Match 98.2%; Score 56; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGL 10
| | | | | | | | | |

```

```

Db 58 RPKPOQFFGL 67

RESULT 4
O97948 PRELIMINARY; PRT; 129 AA.
AC O97948;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Tupala belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50786; CAA90649.1; -.
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 129 AA; 14941 MW; 5855E7ADC2D8674E CRC64;

Query Match 98.2%; Score 56; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGL 10
| | | | | | | | | |
Db 58 RPKPOQFFGL 67

RESULT 5
O9Z0K2 PRELIMINARY; PRT; 97 AA.
AC O9Z0K2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE DELTA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50782; CAA90645.1; -.
DR InterPro; IPR003580; Protachykinin.
DR ProDom; PD005598; Protachykinin; 1.
FT CHAIN 58 68 SUBSTANCE P.
SQ SEQUENCE 97 AA; 11222 MW; FFD50C3297E3F7E3 CRC64;

Query Match 84.2%; Score 48; DB 11; Length 97;
Best Local Similarity 90.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGL 10

```

```

||||| |||
Db 58 RPKPQQSFGL 67

RESULT 6
ID Q920K1 PRELIMINARY; PRT; 115 AA.
AC Q920K1;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoefter M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50783; CAA90646.1; -.
DR InterPro; IPR002040; Tachykinin.
DR ProDom; PD005598; Protachykinin.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
DR CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 83 92 NEUROKININ A.
SQ SEQUENCE 115 AA; 13190 MW; 39EFFB8CBB47174 CRC64;

Query Match 84.2%; Score 48; DB 11; Length 115;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQSFGL 10
||||| |||
Db 58 RPKPQQSFGL 67

RESULT 7
ID Q920K0 PRELIMINARY; PRT; 130 AA.
AC Q920K0;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoefter M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50784; CAA90647.1; -.
DR InterPro; IPR002040; Tachykinin.
DR ProDom; PD005598; Protachykinin.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
DR CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 130 AA; 14850 MW; C4B2F5B6A60A7C0 CRC64;

Query Match 84.2%; Score 48; DB 11; Length 130;
Best Local Similarity 90.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQSFGL 10
||||| |||
Db 58 RPKPQQSFGL 67

RESULT 8
ID Q24014 PRELIMINARY; PRT; 786 AA.
AC Q24014;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE G1-LIKE ORF'S PRODUCT.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DMUC2;
RX MEDLINE=94302132; PubMed=8029320;
RA Kiyosawa H., Hughes J.E., Welker D.L.;
RT "Compatible Dictyostelium mucoroides nuclear plasmids Dmp1 and Dmp2
both belong to the Ddpl plasmid family.";
RL Plasmid 31:121-130(1994).
DR EMBL; U00176; AAC14374.1; -.
SQ SEQUENCE 786 AA; 90191 MW; 2167146E1F012003 CRC64;

Query Match 68.4%; Score 39; DB 5; Length 786;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQSFGL 10
||||| |||
Db 717 KPEPIQFFGI 726

RESULT 9
ID Q24012 PRELIMINARY; PRT; 803 AA.
AC Q24012;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE G1-LIKE ORF'S PRODUCT.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DMUC2;
RX MEDLINE=94302132; PubMed=8029320;
RA Kiyosawa H., Hughes J.E., Welker D.L.;
RT "Compatible Dictyostelium mucoroides nuclear plasmids Dmp1 and Dmp2
both belong to the Ddpl plasmid family.";
RL Plasmid 31:121-130(1994).
DR EMBL; U00175; AAC14372.1; -.
SQ SEQUENCE 803 AA; 91385 MW; 219F8272F416FACD CRC64;

Query Match 68.4%; Score 39; DB 5; Length 803;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQSFGL 10
||||| |||
Db 734 KPEPIQFFGI 743

RESULT 10
ID Q20174
```



```
Query Match      66.7%; Score 38; DB 5; Length 235;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
   :|:|:|:|
Db 85 KPQDFMGL 94

RESULT 13
ID Q9SUN5 PRELIMINARY; PRT; 257 AA.
AC Q9SUN5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE SNRNP PROTEIN.
GN F9F13.90 OR A74G20440.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Pohl T., Weizenegger T., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL080253; CAB45810.1; -.
DR EMBL; AL161553; CAB79044.1; -.
DR InterPro; IPR002965; P-rich_extensn.
DR InterPro; IPR001163; snRNP_Sm.
DR Pfam; PF01423; Sm; 1.
DR PRINTS; PR01217; PRICHEXTENS.
SQ SEQUENCE 257 AA; 27140 MW; D931178ECBC51BF5 CRC64;

Query Match      66.7%; Score 38; DB 10; Length 257;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOFFG 9
   |||:|:|
Db 189 RPPQOFFSG 197

RESULT 14
ID Q9V2N2 PRELIMINARY; PRT; 249 AA.
AC Q9V2N2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 29.2 KDA PROTEIN.
GN PAB2321.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN-ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
   structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248283; CAB48966.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 249 AA; 29212 MW; 392F2EC61C84D6FD CRC64;

Query Match      64.9%; Score 37; DB 1; Length 247;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
   ||:|:|:|
Db 124 RIKPEKFFGI 133

RESULT 15
ID P94873 PRELIMINARY; PRT; 3722 AA.
AC P94873;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ALPHA-AMINOADIPYL-CYSTEINYL-VALINE SYNTHETASE.
GN PCBAB.
OS Lysobacter lactamgenus.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonadaceae;
OC Lysobacter.
OX NCBI_TaxID=39596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-YK90;
RX MEDLINE=96275949; PubMed=8737573;
RA Kimura H., Miyashita H., Sumino Y.;
RT "Organization and expression in Pseudomonas putida of the gene cluster
   involved in cephalosporin biosynthesis from Lysobacter lactamgenus
   YK90.";
RL Appl. Microbiol. Biotechnol. 45:490-501(1996).
DR EMBL; D50308; BAA08846.1; -.
DR HSSP; P14687; IAMU.
DR InterPro; IPR002106; AA_tRNA_ligase_II.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR001242; DUF4.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR003880; Phosphopant_attach.
DR InterPro; IPR001031; Thioesterase.
DR Pfam; PF00501; AMP-binding; 3.
DR Pfam; PF00668; Condensation; 3.
DR Pfam; PF00550; pp-binding; 3.
DR Pfam; PF00975; Thioesterase; 1.
DR PROSITE; PS00179; AA_tRNA_LIGASE_II_1; UNKNOWN_1.
DR PROSITE; PS00075; ACP_DOMAIN; 3.
DR PROSITE; PS00455; AMP_BINDING; 1.
DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_2.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_2.
KW Phosphopantetheine.
SQ SEQUENCE 3722 AA; 411611 MW; 3597B3483463809B CRC64;

Query Match      64.9%; Score 37; DB 2; Length 3722;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKPQOFFGL 10
   |||:|:|
Db 1412 PKPDEFGL 1420
```

Search completed: March 15, 2002, 14:31:00
Job time: 579 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:23:49 ; Search time 34.92 seconds
(without alignments)
23.995 Million cell updates/sec

Title: US-09-988-792-13
Perfect score: 57
Sequence: 1 RPKPQQFFGLX 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	98.2	11	1	SPHO	substance P - hors
2	56	98.2	11	1	A60654	substance P - guin
3	56	98.2	63	2	JC2412	tachykinin gamma c
4	56	98.2	72	2	I62742	tachykinin A gamma
5	56	98.2	72	2	JC5455	preprotachykinin-A
6	56	98.2	97	2	S12958	tachykinin delta p
7	56	98.2	112	1	SPRTA	substance P alpha
8	56	98.2	115	1	SPRGG	substance P gamma
9	56	98.2	115	2	S47039	tachykinin 1 precu
10	56	98.2	129	1	SPHOB	neurokinin 1 precu
11	56	98.2	130	1	SPRTB	substance P beta p
12	56	98.2	130	1	SPROB	neurokinin 1 precu
13	56	98.2	130	2	S47038	tachykinin 1 precu
14	56	98.2	130	2	I52526	neurokinin 1 precu
15	53	93.0	11	2	JN0023	substance P - chic
16	45	78.9	11	2	S23308	substance P - rain
17	44	77.2	11	2	S23306	substance P - Atla
18	43	75.4	11	2	S33300	probable substance
19	41	71.9	3628	2	T13857	trithorax protein
20	39	68.4	11	2	F60409	substance P-like p
21	39	68.4	11	2	E60409	substance P-like p
22	39	68.4	12	2	S10059	tachykinin - Afric
23	38	66.7	205	2	T30016	hypothetical prote
24	38	66.7	257	2	T10586	small nuclear ribo
25	37	64.9	249	2	G75189	hypothetical prote
26	36	63.2	11	2	A61033	ranatachykinin A -
27	36	63.2	629	2	T19563	hypothetical prote
28	36	63.2	728	2	E69486	translation elonga
29	35	61.4	133	2	A25777	T-cell receptor be

30	35	61.4	206	2	T33064	hypothetical prote
31	35	61.4	321	2	A64173	conserved hypothet
32	35	61.4	347	2	T05737	probable hordein C
33	35	61.4	373	2	T02976	probable DNA bindi
34	35	61.4	474	2	T15511	hypothetical prote
35	35	61.4	494	2	E86671	lysine--trna ligas
36	35	61.4	512	2	A82296	lysyl-trna synthet
37	35	61.4	832	2	S76815	hypothetical prote
38	34	60.5	216	2	F96657	hypothetical prote
39	34	59.6	167	2	T36290	probable integral
40	34	59.6	306	2	H81036	riboflavin kinase/
41	34	59.6	316	2	T13601	hypothetical prote
42	34	59.6	318	2	A81982	FAD synthase NMA06
43	34	59.6	359	2	T52337	phosphoprotein pho
44	34	59.6	498	1	S48058	cytochrome P450 cy
45	34	59.6	502	2	JX0334	cytochrome P450 3A

ALIGNMENTS

RESULT 1

SPHO
substance P - horse
C:Species: Equus caballus (domestic horse)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C:Accession: A01558
R:Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A:Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pierdedarm.
A:Reference number: A01558
A:Accession: A01558
A:Molecule type: protein
A:Residues: 1-11 <SPU>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; Hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
|||||
Db 1 RPKPQQFFGL 10

RESULT 2

A60654
substance P - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C:Accession: A60654
R:Murphy, R.
Neuropeptides 14, 105-110, 1989
A:Title: Primary amino acid sequence of guinea-pig substance P.
A:Reference number: A60654; MUID:90044685
A:Accession: A60654
A:Molecule type: protein
A:Residues: 1-11 <MUR>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
|||||
Db 1 RPKPQQFFGL 10

RESULT 3

JC2412
tachykinin gamma chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: JC2412
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the rat
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2412
A:Molecule type: mRNA
A:Residues: 1-63 <KHA>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:12-21/Product: substance P #status predicted <SUP>
F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 98.2%; Score 56; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQQFFGL 10
DB 11 RPKPQQFFGL 20
|||||

RESULT 4

162742
tachykinin A gamma chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I62742; JC5453
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287
A:Accession: I62742
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-72 <RES>
A:Cross-references: GB:M68909; NID:g200469; PIDN:AAA39970.1; PID:g554261
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is involved in
C:Genetics:
A:Gene: gamma-ppt-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 98.2%; Score 56; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQQFFGL 10
DB 23 RPKPQQFFGL 32
|||||

RESULT 5

JC5455
preprotachykinin-A gamma precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
C:Accession: JC5455; I45967
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287

A:Accession: JC5455

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-72 <CHI>

A:Cross-references: GB:M68912; NID:g163593; PIDN:AAA30725.1; PID:g552336

C:Comment: This protein contains two tachykinin peptide hormone substance-P which is

C:Genetics:

A:Gene: ppt-A

C:Superfamily: substance P precursor

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-33/Product: substance-P #status predicted <STP>

F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 98.2%; Score 56; DB 2; Length 72;

Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10

DB 23 RPKPQQFFGL 32

|||||

RESULT 6

SI2958
tachykinin delta precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: SI2958; JC2413
R:Harnax, A.J.; Hyde, V.; Chapman, K.
FEBS Lett. 275, 22-24, 1990
A:Title: Identification and cDNA sequence of delta-preprotachykinin, a fourth splicing
A:Reference number: SI2958; MUID:91085565
A:Accession: SI2958
A:Molecule type: mRNA
A:Residues: 1-97 <KHA>

RESULT 7

SPRTA
substance P alpha precursor - rat
N:Alternate names: preprotachykinin alpha
N:Contains: substance P
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: B26590
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and ne
A:Reference number: A94187; MUID:87118268
A:Accession: B26590

Query Match 98.2%; Score 56; DB 2; Length 97.4;

Best Local Similarity 100.0%; Pred. No. 0.0027;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10

DB 58 RPKPQQFFGL 67

|||||

A:Molecule type: mRNA
A:Residues: 1-112 <KRA>
A:Cross-references: GB:M34184; NID:g206329; PIDN:AAA41925.1; PID:g206330
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the alpha and beta forms.
C:Comment: The alpha form is processed to yield substance P.
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F:1-112/Product: substance P alpha precursor #status predicted <SIG>
F:1-15/Domain: signal sequence #status predicted <SBP>
F:58-68/Product: substance P #status predicted <SBP>
F:66/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycosylation)

Query Match 98.2%; Score 56; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
|||||
Db 58 RPKPQQFFGL 67

RESULT 8
SPRBG
substance P gamma precursor - rabbit
N:Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykinin
N:Contains: neurokinin A; neuropeptide K; substance P
C:Species: Oryzolaque cuniculus (domestic rabbit)
C:Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: JN0709; A60302; A60200; S18922
C:Maegert, H.J.; Heitland, A.; Rose, M.; Forssmann, W.G.
Biochem. Biophys. Res. Commun. 195, 128-131, 1993
A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.
A:Reference number: JN0709; MUID:93371392
A:Accession: JN0709
A:Molecule type: mRNA
A:Residues: 1-115 <MA2>
A:Cross-references: EMBL:X62994; NID:g1565; PIDN:CAA44728.1; PID:g1566
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
Regul. Pept. 18, 346, 1987
A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived from gamma-aminobutyric acid.
A:Reference number: A60302
A:Accession: A60302
A:Molecule type: protein
A:Residues: 72-92 <KAG>
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
J. Neurochem. 50, 1412-1417, 1988
A:Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived from gamma-aminobutyric acid.
A:Reference number: A60200; MUID:88199570
A:Accession: A60200
A:Molecule type: protein
A:Residues: 72-92 <KA2>
C:Comment: The gamma alternatively spliced form is processed to yield substance P and neuropeptide K.
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:72-92/Product: gamma-neuropeptide K #status predicted <NPK>
F:83-92/Product: neurokinin A #status predicted <NKA>
F:66/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycosylation)

Query Match 98.2%; Score 56; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
|||||
Db 58 RPKPQQFFGL 67

RESULT 9

S47039
tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47039
R:Heitland, A.; Kruhoffer, M.; Juergen Maegert, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47039
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <HEI>
A:Cross-references: EMBL:X80663; NID:g520938; PIDN:CAA56692.1; PID:g520939
C:Superfamily: substance P precursor

Query Match 98.2%; Score 56; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
|||||
Db 58 RPKPQQFFGL 67

RESULT 10
SPHUB
neurokinin 1 precursor, beta splice form [validated] - human
N:Alternate names: neurokinin A; neurokinin alpha; neuromedin L; neuropeptide K; prep
N:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 pre
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1988 #sequence_revision 26-May-1995 #text_change 19-May-2000
C:Accession: A24805; A60425; S00069; S03033; JC5451; JC5450; A59269; A59270; B59270;
R:Harmar, A.J.; Armstrong, A.; Pascall, J.C.; Chapman, K.; Rosie, R.; Curtis, A.; Goll
FEBS Lett. 208, 67-72, 1986
A:Title: cDNA sequence of human beta-preprotachykinin, the common precursor to substa
A:Reference number: A24805; MUID:87030957
A:Accession: A24805
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: GB:M28109; EMBL:X54469; NID:g29482; PIDN:CAA38351.1; PID:g29483
R:McGregor, G.P.; Conlon, J.M.
Peptides 11, 907-910, 1990
A:Title: Characterization of the C-terminal flanking peptide of human beta-preprotach
A:Reference number: A60425; MUID:91133994
A:Accession: A60425
A:Molecule type: protein
A:Residues: 111-126 <MCG>
A:Experimental source: neuroendocrine tumor of adrenal medulla
R:Theodorsson-Norheim, E.; Joernvall, H.; Andersson, M.; Norheim, I.; Oberg, K.; Jac
Eur. J. Biochem. 166, 693-697, 1987
A:Title: Isolation and characterization of neurokinin A, neurokinin A(3-10) and neuro
A:Reference number: S00069; MUID:87275962
A:Accession: S00069
A:Molecule type: protein
A:Residues: 98-107 <THE>
R:Kage, R.; Thim, L.; Creutzfeldt, W.; Conlon, J.M.
Biochem. J. 253, 203-207, 1988
A:Title: Post-translational processing of preprotachykinins. Isolation of protachykin
A:Reference number: S03033; MUID:88339887
A:Accession: S03033
A:Molecule type: protein
A:Residues: 20-30 <KAG>
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwells, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5451
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 36-73, 89-122 <CHI1>
A:Cross-references: GB:M68907; NID:g190292; PIDN:AAA60160.1; PID:g553619
A:Accession: JC5450

A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-86,'P',88-122 <CHI2>
A:Cross-references: GB:M68906; NID:g190290; PIDN:AAA60159.1; PID:g553618
R:Tan, A.; Too, H.P.
submitted to GenBank, October 1995
A:Reference number: A59269
A:Accession: A59269
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-129 <TAN>
A:Cross-references: GB:U37529; NID:g1017792; PIDN:AAA79195.1; PID:g1017793
A:Experimental source: tissue brain cortex
R:Lai, J.P.; Douglas, S.D.; Rappaport, E.; Wu, J.M.; Ho, W.Z.
submitted to GenBank, February 1998
A:Description: Identification of a delta isoform of preprotachykinin mRNA in human monocytes K.
A:Reference number: A59270
A:Accession: A59270
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 36-96,'M',116-118 <LAI1>
A:Cross-references: GB:AF050656; NID:g3098594; PIDN:AAC15702.1; PID:g3098595
A:Experimental source: alpha splice form; tissue blood; tissue brain; cell type monocytes K.
A:Accession: B59270
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 36-73,89-96,'M',116-122 <LAT2>
A:Cross-references: GB:AF050658; NID:g3098598; PIDN:AAC15704.1; PID:g3098599
A:Experimental source: delta splice form; tissue blood; tissue brain; cell type monocytes K.
Comment: This protein is processed to produce the tachykinin peptide hormones neurokinin C; Genetics:
A:Gene: GDB:TAC2; NKNA: PPT-A
A:Cross-references: GDB:119452; OMIM:162320
A:Map position: 7q21-q22
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F:1-129/Product: neurokinin 1 precursor, beta splice form #status predicted <SPB>
F:1-96,'M',116-118/Product: neurokinin 1 precursor, alpha splice form #status predicted <SPB>
F:1-73,89-129/Product: neurokinin 1 precursor, gamma splice form #status predicted <SPC>
F:1-73,89-96,'M',116-122/Product: neurokinin 1 precursor, alpha splice form #status predicted <SIG>
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status experimental <NK1>
F:72-107/Product: neuropeptide K #status predicted <NEK>
F:98-107/Product: neurokinin 2 #status experimental <NK2>
F:100-107/Product: neurokinin 2(3-10) #status experimental <NK23>
F:101-107/Product: neurokinin 2(4-10) #status experimental <NK24>
F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycosylation)
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycosylation)

Query Match 98.2% Score 56; DB 1; Length 129;
Best Local Similarity 100.0%; Pred No. 0.0035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQPFGL 10
|||||
Db 58 RPKPQQPFGL 67

RESULT 11
SPRFB
substance P beta precursor - rat
N:Alternate names: preprotachykinin beta; preprotachykinin gamma; substance K
N:Contains: neurokinin A; substance P; substance P gamma precursor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: A37163; A46590; C26590; A25067; J02411
R:Cartier, M.S.; Krause, J.E.
J. Neurosci. 10, 2203-2214, 1990
A:title: Structure, expression, and some regulatory mechanisms of the rat preprotachykinin

A:Reference number: A37163; MUID:90331040
A:Accession: A37163
A:Molecule type: DNA
A:Residues: 1-130 <CAR>
A:Cross-references: GB:M34159; GB:M34160; GB:M34162; NID:g206334; PIDN:AAA41926.1; PT:1
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neurokinin B
A:Reference number: A94187; MUID:87118268
A:Accession: A26590
A:Molecule type: mRNA
A:Residues: 1-130 <KRA>
A:Cross-references: GB:M15191; NID:g2063341; PIDN:AAA41928.1; PID:g206342; GB:M35277
A:Accession: C26590
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KR2>
A:Cross-references: GB:M34183; NID:g206343; PIDN:AAA41929.1; PID:g206344
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of two alternative splicing forms
A:Reference number: A25067; MUID:87025808
A:Accession: A25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
A:Cross-references: GB:M14312; NID:g206339; PIDN:AAA41927.1; PID:g206340
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the rat brain
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2411
A:Molecule type: mRNA
A:Residues: 48-110 <KHA>
A:Experimental source: intestine
A:Comment: Alternative splicing of the mRNA for substance P precursor yields the beta and gamma forms
A:Comment: The beta and gamma forms are processed to yield substance P and neurokinin C/Genetics:
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
A:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F:1-130/Product: substance P beta precursor #status predicted <PREB>
F:1-73, 89-130/Product: substance P gamma precursor #status predicted <PREG>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:98-107/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 98.2%; Score 56; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RPKPQQPFGL 10
|||||
Db 58 RPKPQQPFGL 67
|||||
RESULT 12
SPBOB
N:Alternate names: neurokinin, beta splice form [validated] - bovine
N:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 pre
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Jun-2000
C:Accession: A05093; A01559; A01557; B25067; A61460; JC5454; I45966
R:Nawa, H.; Kotani, H.; Nakanishi, S.
Nature 312, 729-734, 1984
A:Title: Tissue-specific generation of two preprotachykinin mRNAs from one gene by al
A:Reference number: A05093; MUID:85086245
A:Accession: A05093
A:Molecule type: DNA
A:Residues: 1-130 <NAW1>
A:Cross-references: GB:M02351; GB:M14786; NID:g655; PIDN:CAA26206.1; PID:q1197197

A;Residues: 1-130 <NAWL>

R:Nawa, H.; Hirose, T.; Takashima, H.; Inayama, S.; Nakanishi, S.
Nature 306, 32-36, 1983
A:Title: Nucleotide sequences of cloned cDNAs for two types of bovine brain substance P
A:Reference number: A93318; MUID:84039802
A:Accession: A01559
A:Molecule type: mRNA
A:Residues: 1-130 <NAW2>
A:Cross-references: GB:X00075; NID:g758; PIDN:CAA24939.1; PID:g759
A:Accession: A01557
A:Molecule type: mRNA
A:Residues: 1-96, 'M', 116-130 <NAW3>
A:Cross-references: GB:X00076; NID:g762; PIDN:CAA24942.1; PID:g763
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of a
A:Reference number: A25067; MUID:87025808
A:Accession: B25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <XAW>
R:McGregor, G.P.; Kage, R.; Thim, L.; Conlon, J.M.
J. Neurochem. 53, 1871-1877, 1989
A:Title: Quantitation and characterization of peptides from the C-terminal flanking region
A:Reference number: A61460; MUID:90039314
A:Accession: A61460
A:Molecule type: protein
A:Residues: 111-126 <MCG>
A:Experimental source: Corpus striatum
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5454
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-120, 'A', 122 <CHI>
A:Cross-references: GB:M68911; NID:gl63591; PIDN:AAA30724.1; PID:g552335
A:Comment: The protein is processed to produce neurokinin 1 (substance P) and neurokinin
C:Genetics:
A:Gene: PPT-A
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
A:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F:1-130/Product: neurokinin 1 precursor, beta splice form #status predicted <SPB>
F:1-96, 'M', 116-130/Product: neurokinin 1 precursor, alpha splice form #status predicted
F:1-73, 89-130/Product: neurokinin 1 precursor, gamma splice form #status predicted <SPC>
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status experimental <SBP>
F:98-107/Product: neurokinin 2 #status predicted <NEK>
F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 98.2%; Score 56; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
| | | | | | | | | |
Db 58 RPKPQQFFGL 67

RESULT 13

S47038
tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47038
R:Heitland, A.; Kruhoffer, M.; Juergen Maegert, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47038

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <HEI>
A:Cross-references: EMBL:X80662; NID:g520917; PIDN:CAA56691.1; PID:g520918
C:Superfamily: substance P precursor

Query Match 98.2%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
| | | | | | | | | |
Db 58 RPKPQQFFGL 67

RESULT 14

I52526
neurokinin 1 precursor - mouse
N:Alternate names: neurokinin A; preprotachykinin; substance P; substance P
N:Contains: neurokinin 1; neurokinin 2
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000
C:Accession: I52526; JC5452; I62741
R:Kako, K.; Munekata, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A:Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and
A:Reference number: I52526
A:Accession: I52526
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-130 <KAK>
A:Cross-references: GB:D17584; NID:g407345; PIDN:BAA04508.1; PID:g435121
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5452
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 36-122 <CHI>
A:Cross-references: GB:M68908; NID:g200467; PIDN:AAA39969.1; PID:g554260
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status predicted <NK1>
F:98-107/Product: neurokinin 2 #status predicted <NK2>
F:111-126/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 98.2%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
| | | | | | | | | |
Db 58 RPKPQQFFGL 67

RESULT 15

JN0023
substance P - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C:Accession: JN0023
R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A:Reference number: JN0023; MUID:88204263
A:Accession: JN0023
A:Molecule type: protein
A:Residues: 1-11 <CON>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 93.0%; Score 53; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.0011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	RPKPOQFFGL	10
Db	1	RPRPOQFFGL	10

Search completed: March 15, 2002, 14:23:49
Job time: 223 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:23:06 ; Search time 32.16 Seconds
(without alignments)
7.697 Million cell updates/sec

Title: US-09-988-792-13
Perfect score: 57
Sequence: 1 RPKPQQFFGLX 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS-COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	98.2	11	1 US-07-934-553-1	Sequence 1, Appli
2	56	98.2	11	1 US-08-031-325A-26	Sequence 26, Appl
3	56	98.2	11	1 US-08-184-935-12	Sequence 12, Appl
4	56	98.2	11	1 US-08-269-288-2	Sequence 2, Appli
5	56	98.2	11	1 US-08-338-484-1	Sequence 1, Appli
6	56	98.2	11	1 US-08-175-432-1	Sequence 1, Appli
7	56	98.2	11	1 US-08-225-474-1	Sequence 1, Appli
8	56	98.2	11	1 US-08-391-910-2	Sequence 2, Appli
9	56	98.2	11	1 US-08-418-994-2	Sequence 2, Appli
10	56	98.2	11	1 US-08-480-505-3	Sequence 3, Appli
11	56	98.2	11	1 US-08-391-814-2	Sequence 2, Appli
12	56	98.2	11	1 US-08-167-870-1	Sequence 1, Appli
13	56	98.2	11	1 US-08-255-272-6	Sequence 6, Appli
14	56	98.2	11	1 US-08-441-591-6	Sequence 6, Appli
15	56	98.2	11	1 US-08-303-362A-6	Sequence 6, Appli
16	56	98.2	11	1 US-08-462-859A-1	Sequence 1, Appli
17	56	98.2	11	1 US-08-123-659A-1	Sequence 1, Appli
18	56	98.2	11	1 US-08-462-415-2	Sequence 2, Appli
19	56	98.2	11	1 US-08-463-874-2	Sequence 2, Appli
20	56	98.2	11	1 US-08-464-247A-1	Sequence 1, Appli
21	56	98.2	11	1 US-08-464-248A-1	Sequence 1, Appli
22	56	98.2	11	1 US-08-444-135-2	Sequence 2, Appli
23	56	98.2	11	1 US-08-318-391-2	Sequence 2, Appli
24	56	98.2	11	2 US-08-796-598-11	Sequence 11, Appl
25	56	98.2	11	2 US-08-447-175A-11	Sequence 11, Appl
26	56	98.2	11	2 US-07-737-371E-13	Sequence 13, Appl
27	56	98.2	11	2 US-07-737-371E-14	Sequence 14, Appl

28	56	98.2	11	2 US-07-737-371E-63	Sequence 63, Appl
29	56	98.2	11	2 US-07-737-371E-64	Sequence 64, Appl
30	56	98.2	11	2 US-07-737-371E-77	Sequence 77, Appl
31	56	98.2	11	2 US-08-848-766A-1	Sequence 1, Appli
32	56	98.2	11	2 US-08-747-137-34	Sequence 34, Appl
33	56	98.2	11	3 US-08-927-128-17	Sequence 2, Appli
34	56	98.2	11	4 US-08-257-966-2	Sequence 34, Appl
35	56	98.2	11	4 US-08-505-250-34	Sequence 23, Appl
36	56	98.2	11	5 PCT-US95-05600-23	Patent No. 5441935
37	56	98.2	11	6 5441935-1	Sequence 7, Appli
38	56	98.2	12	1 US-08-441-591-7	Sequence 7, Appli
39	56	98.2	12	1 US-08-303-362A-7	Sequence 27, Appl
40	56	98.2	12	4 US-08-505-250-27	Sequence 53, Appl
41	56	98.2	12	4 US-08-505-250-53	Sequence 4, Appli
42	56	98.2	12	5 PCT-US92-06532-4	Sequence 24, Appl
43	56	98.2	12	5 PCT-US95-05600-24	Sequence 2, Appli
44	56	98.2	20	3 US-08-890-157A-2	Sequence 50, Appl
45	56	98.2	20	4 US-08-505-250-50	

ALIGNMENTS

RESULT 1
US-07-934-553-1
; Sequence 1, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING Ige
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLOM, LUNGUMUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,553
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-9033CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-934-553-1

Query Match 98.2% Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10

```
Db      1 RPKPQQFFGL 10
|||||
RESULT  2
US-08-031-325A-26
; Sequence 26, Application US/08031325A
; Patent No. 5369094
; GENERAL INFORMATION:
; APPLICANT: Schally, Andrew V.
; APPLICANT: Cal, Renzhi
; TITLE OF INVENTION: POLYPEPTIDE BOMBESIN ANTAGONISTS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OMRI M. BEHR, ESQ
; STREET: 325 PIERSON AVENUE
; CITY: EDISON
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 08837
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,325A
; FILING DATE: 15-MAR-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,747
; FILING DATE: 29-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BEHR, OMRI M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 494-5240
; TELEFAX: (908) 494-0428]
; TELEX: 511642 BEPATDIN
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: /note= "Res 11 = Met-NH2"
;
US-08-031-325A-26
Query Match      98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RPKPQQFFGL 10
|||||
Db      1 RPKPQQFFGL 10
|||||
RESULT  3
US-08-184-935-12
; Sequence 12, Application US/08184935
; Patent No. 5476770
; GENERAL INFORMATION:
; APPLICANT: PRADELLES, PHILIPPE
; TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN
; TITLE OF INVENTION: OR HAPTEN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,935
; FILING DATE: 24-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5476770man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 846-286-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "C-terminal amide"
;
US-08-184-935-12
Query Match      98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RPKPQQFFGL 10
|||||
Db      1 RPKPQQFFGL 10
|||||
RESULT  4
US-08-269-288-2
; Sequence 2, Application US/08269288
; Patent No. 5451140
; GENERAL INFORMATION:
; APPLICANT: Bruns, Robert F.
; APPLICANT: Gehlert, Donald R.
; APPLICANT: Howbert, James J.
; APPLICANT: Lunn, William H.W.
; TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANT. HISTY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,288
; FILING DATE:
; CLASSIFICATION: 514
```

ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9715
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-269-288-2

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
| | | | | | | | | |
DB 1 RPKPQOFFGL 10

RESULT 5
US-08-338-484-1
Sequence 1, Application US/08338484
Patent No. 5494926
GENERAL INFORMATION:
APPLICANT: Owens, Andrew P.
APPLICANT: Teall, Martin R.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: 2/3-(HETEROCYCLIC ALKYL
TITLE OF INVENTION: AMINO)-1-(SUBSTITUTED PHENYL-METHOXY)-ETHANES/PROPANES AS
TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Robert J. No. 5494926th
STREET: 126 E. Lincoln Ave., P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,484
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: NO. 5494926th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-484-1

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQOFFGL 10
| | | | | | | | | |
DB 1 RPKPQOFFGL 10
| | | | | | | | | |
RESULT 6
US-08-175-432-1
Sequence 1, Application US/08175432
Patent No. 5495047
GENERAL INFORMATION:
APPLICANT: Saari, Walfred S.
APPLICANT: Van Niel, Monique B.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: FUSED TRICYCLIC COMPOUNDS.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE
TITLE OF INVENTION: IN THERAPY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NORTH, ROBERT J.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,432
FILING DATE: 07-JAN-1994
CLASSIFICATION: 560

ATTORNEY/AGENT INFORMATION:
NAME: NO. 5495047th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1152Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-175-432-1

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
| | | | | | | | | |
DB 1 RPKPQOFFGL 10

RESULT 7
US-08-225-474-1
Sequence 1, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
APPLICANT: Patterson, Roy
APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: Ige Mediated Allergies
NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 S. Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,474
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,553
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.
; REGISTRATION NUMBER: 16,926
; REFERENCE/DOCKET NUMBER: NU 9033-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-225-474-1

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
Db 1 RPKPQOFFGL 10

RESULT 8
US-08-391-910-2
; Sequence 2, Application US/08391910
; Patent No. 5363133
; GENERAL INFORMATION:
; APPLICANT: Hipskind, Philip A.
; TITLE OF INVENTION: HEXAMETHYLENIMINYL TACHYKININ RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,910
; FILING DATE:
; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9979
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-910-2

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
Db 1 RPKPQOFFGL 10

RESULT 9
US-08-418-994-2
; Sequence 2, Application US/08418994
; Patent No. 5565568
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung-Yong S.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, J. J.
; APPLICANT: Muehl, Brian S.
; APPLICANT: Nixon, James A.
; TITLE OF INVENTION: 2-ACYLAMINOPROPANAMIDES AS TACHYKININ
; TITLE OF INVENTION: RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,994
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-418-994-2

Query Match 98.2%; Score 56; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGL 10
| | | | | | | |
Db 1 RPKPQQFFGL 10

RESULT 10
US-08-480-505-3
; Sequence 3, Application US/08480505
; Patent No. 5601821
; GENERAL INFORMATION:
; APPLICANT: STAMWORTH, DENIS R
; APPLICANT: LEWIN, IAN V
; APPLICANT: NAYAR, SARITA
; APPLICANT: JONES, VALERIE
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-3360
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,505
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,692
; FILING DATE:
; APPLICATION NUMBER: US 07/776,380
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: GB 8913737.6
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB90/00926
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 875-0400
; TELEFAX: (703) 525-3468
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Neuropeptide "Substance P"
; US-08-480-505-3

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGL 10
| | | | | | | |
Db 1 RPKPQQFFGL 10

RESULT 11
US-08-391-814-2
; Sequence 2, Application US/08391814
; Patent No. 5607947
; GENERAL INFORMATION:
; APPLICANT: Hipskind, Phillip A.
; TITLE OF INVENTION: PYRROLIDINYL TACHYKININ RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,814
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-814-2

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPQQFFGL 10
| | | | | | | |
Db 1 RPKPQQFFGL 10

RESULT 12
US-08-167-870-1
; Sequence 1, Application US/08167870
; Patent No. 5610183
; GENERAL INFORMATION:
; APPLICANT: OWENS, ANDREW P.
; APPLICANT: WILLIAMS, BRIAN J.
; TITLE OF INVENTION: AROMATIC COMPOUNDS, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM AND THEIR USE IN THERAPY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERT J. NORTH
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/167,870
;; FILING DATE: 17-DEC-1993
;; CLASSIFICATION: 544
;; ATTORNEY/AGENT INFORMATION:
;; NAME: NORTH, ROBERT J.
;; REGISTRATION NUMBER: 27,366
;; REFERENCE/DOCKET NUMBER: T-1151Y
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (908)594-7262
;; TELEFAX: (908)594-4720
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-167-870-1

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
|||||
DB 1 RPKPQOFFGL 10

RESULT 13

US-08-255-272-6
;; Sequence 6, Application US/08255272
;; Patent No. 5627268
;; GENERAL INFORMATION:
;; APPLICANT: Kumar, Ramesh
;; APPLICANT: Sharma, Ajay
;; APPLICANT: Khoury-Christianson, Anastasia
;; APPLICANT: M.
;; TITLE OF INVENTION: Production of Therapeutic Peptides in
;; NUMBER OF INVENTION: Transgenic Animals as a Fusion with Hemoglobin
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PENNIE & EDMONDS
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/255,272
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30742
;; REFERENCE/DOCKET NUMBER: 6794-032
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid

;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-255-272-6

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
|||||
DB 1 RPKPQOFFGL 10

RESULT 14

US-08-441-591-6
;; Sequence 6, Application US/08441591
;; Patent No. 5637682
;; GENERAL INFORMATION:
;; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
;; TITLE OF INVENTION: HIGH-AFFINITY
;; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
;; TITLE OF INVENTION: TO THE TACHYKININ
;; TITLE OF INVENTION: SUBSTANCE P
;; NUMBER OF SEQUENCES: 66
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Swanson & Bratschun, L.L.C.
;; STREET: 8400 E. Prentice Avenue, Suite 200
;; CITY: Englewood
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/441,591
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/303,362
;; FILING DATE: 9-SEPTEMBER-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/714,131
;; FILING DATE: 10-JUNE-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/931,473
;; FILING DATE: 17-AUGUST-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/117,991
;; FILING DATE: 8-SEPTEMBER 1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/536,428
;; FILING DATE: 11-JUNE-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/964,624
;; FILING DATE: 21-OCTOBER-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barry J. Swanson
;; REGISTRATION NUMBER: 33,215
;; REFERENCE/DOCKET NUMBER: NEX21/C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 793-3333
;; TELEFAX: (303) 793-3433
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11
;; TYPE: amino acid
;; STRANDEDNESS: single

TOPOLOGY: linear
US-08-441-591-6

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
| | | | | | | | | |
Db 1 RPKPQOFFGL 10

RESULT 15

US-08-303-362A-6
; Sequence 6, Application US/08303362A
; Patent No. 5648214

GENERAL INFORMATION:

APPLICANT: NEUWLANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

STREET: Swanson & Bratschun, L.L.C.

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,362A

FILING DATE: 9-SEPTEMBER-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991

FILING DATE: 8-SEPTEMBER 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX21

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 11

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-303-362A-6

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10

| | | | | | | | | |

Db 1 RPKPQOFFGL 10

Search completed: March 15, 2002, 14:23:06
Job time: 216 sec

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00046;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:32:20 ; Search time 20.4 Seconds
(without alignments)
19.770 Million cell updates/sec

Title: US-09-988-792-13
Perfect score: 57
Sequence: 1 RPKPQQFFGLX 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	56	98.2	11	1 TKNA_HORSE	P01290 equus cabal
2	56	98.2	115	1 TKN1_RABIT	P41540 oryctolagus
3	56	98.2	129	1 TKN1_HUMAN	P20366 homo sapien
4	56	98.2	130	1 TKN1_BOVIN	P01289 bos taurus
5	56	98.2	130	1 TKN1_MESAU	Q60541 mesocricetu
6	56	98.2	130	1 TKN1_MOUSE	P41539 mus musculus
7	56	98.2	130	1 TKN1_RAT	P06767 rattus norv
8	53	93.0	11	1 TKNA_CHICK	P19850 gallus gall
9	45	78.9	11	1 TKNA_ONCMY	P28499 oncorhynch
10	44	77.2	11	1 TKNA_GADMO	P28498 gadus morhu
11	43	75.4	11	1 TKNA_SCYCA	P41333 scylliorhinu
12	41	71.9	3828	1 TRX_DROVI	Q24742 drosophila
13	39	68.4	11	1 TKN4_PSEGU	P42989 pseudophryn
14	39	68.4	11	1 TKN5_PSEGU	P42990 pseudophryn
15	39	68.4	12	1 TKN1_KASMA	P08613 kassina mac
16	38	66.7	11	1 TKN1_RANRI	P29207 rana ridibu
17	36	63.2	11	1 TKNA_RANCA	P22688 rana catesb
18	36	63.2	167	1 SERO_GALME	Q76192 gallieria me
19	36	63.2	728	1 EF2_ARCFU	Q28385 archaeglob
20	35	61.4	313	1 ISPE_HAEIN	P45271 haemophilus
21	35	61.4	512	1 SYK_VIBCH	Q9ku60 vibrio chol
22	35	61.4	757	1 RELA_MYXXA	O52177 myxococcus
23	34	59.6	498	1 C6B1_PAPPO	Q04552 papilio pol
24	34	59.6	503	1 CP3A_MESAU	Q64148 mesocricetu
25	34	59.6	504	1 CP31_RAT	P04800 rattus norv
26	34	59.6	585	1 PPOF_LYCES	Q08296 lycopersico
27	34	59.6	587	1 PPOB_LYCES	Q08307 lycopersico
28	34	59.6	588	1 PPOB_SOLTU	Q06355 solanum tub
29	34	59.6	1799	1 Y025_CAEEL	P34675 caenorhabdi
30	33	57.9	282	1 YKCO_CAEEL	P42001 caenorhabdi
31	33	57.9	404	1 CAG5_CHICK	Q92184 gallus gall
32	33	57.9	420	1 CRF1_CHICK	Q90812 gallus gall
33	33	57.9	495	1 SYK_STAAU	Q53638 staphylococ

RESULT 1

ID	TKNA_HORSE	STANDARD;	PRT;	11 AA.
AC	P01290;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	SUBSTANCE P.			
GN	TAC1 OR NKNA OR TAC2 OR NKA.			
OS	Equus caballus (Horse), and Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796, 10141;			
RN	[1]			
RP	SEQUENCE.			
RC	SPECIES=Horse;			
RA	Studer R.O., Trzeciak A., Lergier W.;			
RT	"Isolation and amino-acid sequence of substance P from horse			
RT	intestine.";			
RL	Helv. Chim. Acta 56:860-866(1973).			
RN	[2]			
RP	SEQUENCE.			
RC	SPECIES=C. porcellus;			
RX	MEDLINE=90044685; PubMed=2478925;			
RA	Murphy R.;			
RT	"Primary amino acid sequence of guinea-pig substance P.";			
RL	Neuropeptides 14:105-110(1989).			
CC	-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,			
CC	EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND			
CC	SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH			
CC	MUSCLES.			
CC	-!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.			
DR	PIR; A01558; SPHO.			
DR	PIR; A06654; A60654.			
DR	InterPro: IPR003580; Protachykinin.			
DR	InterPro: IPR002040; Tachykinin.			
DR	Pfam: PF02202; Tachykinin; 1.			
DR	SMART; SM00203; TK; 1.			
DR	SMART; PS00267; TACHYKININ; 1.			
KW	Tachykinin; Neuropeptide; Amidation; Neurotransmitter.			
FT	MOD_RES 11 11			
SQ	SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;			

Query Match 98.2%; Score 56; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
Db 1 RPKPQQFFGL 10

RESULT 2

ID	TKN1_RABIT	STANDARD;	PRT;	115 AA.
----	------------	-----------	------	---------

AC P41540;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE GAMMA; C-TERMINAL
 DE FLANKING PEPTIDE]
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93371392; PubMed=8363593;
 RA Maegert H.J., Heitland A., Rose M., Forssmann W.G.;
 RT "Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.";
 RL Biochem. Biophys. Res. Commun. 195:128-131(1993).
 RN [2]
 RN SEQUENCE OF 72-92.
 RA Kage R., McGregor G.P., Thim L., Conlon J.M.;
 RT "Gamma-neuropeptide K: a peptide isolated from rabbit gut that is
 RT derived from gamma-preprotachykinin.";
 RL Regul. Pept. 18:346-346(1987).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X62994; CAA44728.1; .
 DR PIR; S18922; S18922.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR ProDom; PD005598; Protachykinin; 1.
 DR SMART; SM00203; TK; 2.
 DR PROSITE; PS00267; TACHYKININ; 2.
 KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19 POTENTIAL.
 FT PEPTIDE 20 56 POTENTIAL.
 FT PEPTIDE 58 68 SUBSTANCE P.
 FT PEPTIDE 72 92 NEUROPEPTIDE GAMMA.
 FT PEPTIDE 83 92 NEUROKININ A.
 FT PEPTIDE 96 111 C-TERMINAL FLANKING PEPTIDE.
 FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD_RES 92 92 AMIDATION (G-93 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 115 AA: 13370 MW; 5EC76F7C9B10E1C6 CRC64;
 Query Match 98.2%; Score 56; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RPKPQOFFGL 10
 Db 58 RPKPQOFFGL 67
 RESULT 3
 TKN1_HUMAN

TKN1_HUMAN STANDARD; PRT; 129 AA.
 P20366; Q00072; Q06000; Q06001;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM BETA).
 RX MEDLINE=87030957; PubMed=3770210;
 RA Harnar A.J., Armstrong A., Pascali J.C., Chapman K., Rosie R.,
 RA Curtis A., Goring J., Edwards C.R.W., Fink G.;
 RT "cDNA sequence of human beta-preprotachykinin, the common precursor
 RT to substance P and neurokinin A.";
 RL FEBS Lett. 208:67-72(1986).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM BETA).
 RC TISSUE=Brain;
 RA Tan A., Too H.P.;
 RN Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE=Testis;
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chikwaka C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
 RA Ivell R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 RT human and mouse testis.";
 RL Endocrinology 128:2441-2448(1991).
 RN [4]
 RN SEQUENCE OF 98-107.
 RX MEDLINE=87275962; PubMed=3038549;
 RA Theodorsson-Norheim E., Joernvall H., Andersson M., Norheim I.,
 RA Oberg K., Jacobsson G.;
 RT "Isolation and characterization of neurokinin A, neurokinin A(3-10)
 RT and neurokinin A(4-10) from a neutral water extract of a metastatic
 RT ileal carcinoid tumour.";
 RL Eur. J. Biochem. 166:693-697(1987).
 RN [5]
 RN SEQUENCE OF 36-118 FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Blood, and Brain;
 RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
 RT "Identification of a delta isoform of preprotachykinin mRNA in human
 RT mononuclear phagocytes and lymphocytes.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE OF 111-126.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=91133994; PubMed=2284201;
 RA McGregor G.P., Conlon J.M.;
 RT "Characterization of the C-terminal flanking peptide of human
 RT beta-preprotachykinin.";
 RL Peptides 11:907-910(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC

or send an email to license@isb-sib.ch).

```

CC EMBL; X54469; CAA38351.1; -
CC EMBL; U37529; AAA79195.1; -
CC EMBL; M68906; AAA60159.1; -
CC EMBL; M68907; AAA60160.1; -
CC EMBL; AF050656; AAC15702.1; -
CC EMBL; AF050658; AAC15704.1; -
CC PIR; A24805; A24805.
CC PIR; S00069; S00069.
CC MIM; 162320; -
CC InterPro; IPR003580; Protachykinin.
CC InterPro; IPR002040; Tachykinin.
CC Pfam; PF02202; Tachykinin; 1.
CC ProDom; PD005598; Protachykinin; 1.
CC SMART; SM00203; TK; 2.
CC PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 SUBSTANCE P.
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE K.
FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 98 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE.
FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM
FT DELTA).
FT VARSPPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM
FT DELTA).
FT VARSPPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM
FT DELTA).
FT CONFLICT 87 87 L -> P (IN REF. 4).
FT SEQUENCE 129 AA; 15003 MW; 51412C1692368DE4 CRC64;

Query Match 98.2%; Score 56; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
Db 58 RPKPQQFFGL 67
|||||||

RESULT 4
TKN1_BOVIN STANDARD; PRT; 130 AA.
AC P01289; P01291; P04091; P20773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=85086245; PubMed=6083453;
RA Nawa H., Kotani H., Nakanishi S.;
RT "Tissue-specific generation of two preprotachykinin mRNAs from one
RL gene by alternative RNA splicing.";
RL Nature 312:729-734(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).

```

```

RX MEDLINE=84039802; PubMed=6195531;
RA Nawa H., Hirose T., Takashima H., Inayama S., Nakanishi S.;
RT "Nucleotide sequences of cloned cDNAs for two types of bovine brain
RT substance P precursor.";
RL Nature 306:32-36(1983).
RN [3]
RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RC TISSUE-Hypothalamus;
RX MEDLINE=91209287; PubMed=1708336;
RA Chiwakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Ivell R.;
RT "Tachykinin (substance-P) gene expression in Leydig cells of the
RT human and mouse testis.";
RL Endocrinology 128:2441-2448(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X00075; CAA24939.1; -
CC EMBL; X00075; CAA24940.1; -
CC EMBL; X00075; CAA24941.1; -
CC EMBL; X00076; CAA24942.1; -
CC EMBL; X00076; CAA24943.1; ALT_SEQ.
CC EMBL; X02351; CAA26206.1; -
CC EMBL; X01396; CAA26206.1; JOINED.
CC EMBL; X01397; CAA26206.1; JOINED.
CC EMBL; X01398; CAA26206.1; JOINED.
CC EMBL; X01399; CAA26206.1; JOINED.
CC EMBL; X01400; CAA26206.1; JOINED.
CC EMBL; M68911; AAA30724.1; -
CC EMBL; M68912; AAA30725.1; -
CC PIR; A01557; SPBOA.
CC PIR; A01559; SPBOB.
CC PIR; A05093; A05093.
CC PIR; B25067; B25067.
CC InterPro; IPR003580; Protachykinin.
CC InterPro; IPR002040; Tachykinin.
CC Pfam; PF02202; Tachykinin; 1.
CC ProDom; PD005598; Protachykinin; 1.
CC SMART; SM00203; TK; 2.
CC PROSITE; PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 56 SUBSTANCE P.
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE K.
FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 98 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM
FT DELTA).
FT VARSPPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM
FT DELTA).
FT VARSPPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM
FT DELTA).
FT CONFLICT 121 121 V -> A (IN REF. 3).
FT SEQUENCE 130 AA; 15076 MW; CE2A28572305DEB7 CRC64;
SQ

```

2P187,
A185

Query Match 98.2%; Score 56; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. NO. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 | | | | | | | | | |
 DB 58 RPKPQOFFGL 67

RESULT 5
 TKNL_MESAU
 ID TKNL_MESAU STANDARD; PRT; 130 AA.
 AC Q6541; P49110;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC STRAIN=AURA; TISSUE=Brain;
 RA Heitland A., Kruhoffer M., Juergen Maegert H.J., Forssmann W.G.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC

EMBL; X80662; CAA56691.1; -;
 EMBL; X80663; CAA56692.1; -;
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE; PS00267; TACHYKININ; 2.
 DR Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 56 POTENTIAL.
 FT PEPTIDE 58 68 SUBSTANCE P.
 FT PEPTIDE 72 107 NEUROPEPTIDE K.
 FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 1ST PART.
 FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
 FT PEPTIDE 98 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VARSPPLIC 74 88 MISSING (IN ISOFORM GAMMA).
 SQ SEQUENCE 130 AA; 14907 MW; CC92E9371A646F2E CRC64;

Query Match

98.2%; Score 56; DB 1; Length 130;

Best Local Similarity 100.0%; Pred. NO. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 | | | | | | | | | |
 DB 58 RPKPQOFFGL 67

RESULT 6
 TKNL_MOUSE
 ID TKNL_MOUSE STANDARD; PRT; 130 AA.
 AC P41539; Q00073;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=ICR; TISSUE=Brain;
 RA Kako K., Muneoka E., Hosaka M., Murakami K., Nakayama K.,
 RT "Cloning and sequence analysis of mouse cDNAs encoding
 preprotachykinin A and B."
 RL Biomed. Res. 14:253-259(1993).
 RN [2]
 RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE=Brain;
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chiwakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
 RA Ivell R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 human and mouse testis."
 RL Endocrinology 128:2441-2448(1991).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC

This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC

EMBL; D17584; BAA04508.1; -;
 EMBL; M68908; AAA39969.1; -;
 EMBL; M68909; AAA39970.1; -;
 DR MGI:98474; Tacl.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE; PS00267; TACHYKININ; 2.
 DR Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 56 POTENTIAL.
 FT PEPTIDE 58 68 SUBSTANCE P.
 FT PEPTIDE 72 107 NEUROPEPTIDE K.
 FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 1ST PART.
 FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.

FT PEPTIDE 98 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 FT MOD.RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD.RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA).
 SQ SEQUENCE 130 AA; 15045 MW; 7BB8DA15FDE72FF8 CRC64;

Query Match 98.2%; Score 56; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 DB 58 RPKPQOFFGL 67

RESULT 7
 TKNL_RAT STANDARD; PRT; 130 AA.
 AC P06767; P08856; P22356;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
 RX MEDLINE=90331040; PubMed=1695945;
 RA Carter M.S., Krause J.E.;
 RT "Structure, expression, and some regulatory mechanisms of the rat
 RT preprotachykinin gene encoding substance P, neurokinin A,
 RT neuropeptide K, and neuropeptide gamma.";
 RL J. Neurosci. 10:2203-2214(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
 RX MEDLINE=87118268; PubMed=2433692;
 RA Krause J.E., Chirgwin J.M., Carter M.S., Xu Z.S., Hershey A.D.;
 RT "Three rat preprotachykinin mRNAs encode the neuropeptides substance
 RT P and neurokinin A.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:881-885(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=87025808; PubMed=2429656;
 RA Kawaguchi Y., Hoshimaru M., Nawa H., Nakanishi S.;
 RT "Sequence analysis of cloned cDNA for rat substance P precursor:
 RT existence of a third substance P precursor.";
 RL Biochem. Biophys. Res. Commun. 139:1040-1046(1986).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=87025808; PubMed=2429656;
 RA Kawaguchi Y., Hoshimaru M., Nawa H., Nakanishi S.;
 RT "Sequence analysis of cloned cDNA for rat substance P precursor:
 RT existence of a third substance P precursor.";
 RL Biochem. Biophys. Res. Commun. 139:1040-1046(1986).
 RN [5]
 RP SEQUENCE OF 1-41 FROM N.A.
 RX MEDLINE=93192337; PubMed=8448217;
 RA Chapman K.E., Lyons V., Harnar A.J.;
 RT "The sequence of 5' flanking DNA from the rat preprotachykinin gene;
 RT analysis of putative transcription factor binding sites.";
 RL Biochim. Biophys. Acta 1172:361-363(1993).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.

CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M34162; AAA41926.1;
 CC EMBL; M34159; AAA41926.1; JOINED.
 CC EMBL; M34160; AAA41926.1; JOINED.
 CC EMBL; M34161; AAA41926.1; JOINED.
 CC EMBL; M34184; AAA41925.1;
 CC EMBL; M34183; AAA41929.1;
 CC EMBL; M15191; AAA41928.1;
 CC EMBL; M14312; AAA41927.1;
 CC EMBL; L07328; AAA41924.1;
 CC EMBL; X56306; CAA39752.1;
 CC PIR; A26590; A26590.
 CC PIR; B26590; B26590.
 CC PIR; C26590; C26590.
 CC PIR; A37163; A37163.
 CC PIR; S12958; S12958.
 CC InterPro: IPR003580; Protachykinin.
 CC InterPro: IPR002040; Tachykinin.
 CC Pfam: PF02202; Tachykinin; 1.
 CC ProDom: PD005598; Protachykinin; 1.
 CC SMART: SM00203; TK; 2.
 CC PROSITE: PS00267; TACHYKININ; 2.
 CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 CC Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 56 SUBSTANCE P.
 FT PEPTIDE 58 68 NEUROPEPTIDE K.
 FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
 FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 2ND PART.
 FT PEPTIDE 89 107 NEUROKININ A.
 FT PEPTIDE 98 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 FT MOD.RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD.RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM
 FT DELTA).
 FT VARSPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM
 FT DELTA).
 FT VARSPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM
 FT DELTA).
 SQ SEQUENCE 130 AA; 15001 MW; B22FE960DCCD75A CRC64;

Query Match 98.2%; Score 56; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 DB 58 RPKPQOFFGL 67

RESULT 8
 TKNA_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204263; PubMed=2452461;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; JN0023; JN0023.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 93.0%; Score 53; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.00034;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFFGL 10
Db 1 RRPQOFFGL 10

RESULT 9
TKNA_ONCMY STANDARD; PRT; 11 AA.
AC P28499;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
of the cod and trout."
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S23307; S23307.
DR PIR; S23308; S23308.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 78.9%; Score 45; DB 1; Length 11;
Best Local Similarity 70.0%; Pred. No. 0.01;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKPQOFFGL 10
Db 1 KRPQOFFGL 10
RESULT 10
TKNA_GADMO STANDARD; PRT; 11 AA.
AC P28498;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidae;
OC Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
of the cod and trout."
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 77.2%; Score 44; DB 1; Length 11;
Best Local Similarity 70.0%; Pred. No. 0.016;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQOFFGL 10
Db 1 KRPQOFFGL 10

RESULT 11
TKNA_SCYCA STANDARD; PRT; 11 AA.
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eudrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Balment R.J., Conlon J.M.;

RT "Primary structures and biological activities of substance-P-related
RL peptides from the brain of the dogfish, *Scyliorhinus canicula*.";
Eur. J. Biochem. 214:469-474(1993).

CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.

CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR; S33300; S33300.

DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.

FT MOD_RES 11 11 AMIDATION

SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 75.4%; Score 43; DB 1; Length 11;
Best Local Similarity 70.0%; Pred. No. 0.025;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10

DB :|||:||||

1 KPRPGQFFGL 10

RESULT 12

TRX_DROVI

ID TRX_DROVI STANDARD; PRT; 3828 AA.

AC Q24742;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DE 20-AUG-2001 (Rel. 40, Last annotation update)

DE TRITHORAX PROTEIN.

GN TRX.

OS Drosophila virilis (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7244;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-96100387; PubMed-8555104;

RA Tillib S., Sedkov Y., Mizrokhi L., Mazo A.;

RT "Conservation of structure and expression of the trithorax gene

between *Drosophila* virilis and *Drosophila melanogaster*.";

RL Mech. Dev. 53:113-122(1995).

CC -1- FUNCTION: FUNCTIONS IN SEGMENT DETERMINATION THROUGH INTERACTION

WITH GENES OF BITHORAX (BX-C) AND ANTENNAPEDIA (ANT-X) COMPLEXES.

IT CAN BEHAVE AS AN ACTIVATOR OF BX-C.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION

FACTORS.

CC -1- SIMILARITY: CONTAINS 1 'SET' DOMAIN.

CC -1- SIMILARITY: CONTAINS 5 PHD-TYPE ZINC FINGERS.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Z50038; CAA90349.1; -.

DR HSSP; P04002; 1WFA.

DR FlyBase; FBgn0014844; Dvir\trx.

DR InterPro; IPR003889; Flyrich.C.

DR InterPro; IPR003888; Flyrich_N.

DR InterPro; IPR001965; PHD.

DR InterPro; IPR003616; PostSET.

DR InterPro; IPR001214; SET.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00628; PHD; 2.
DR Pfam; PF00856; SET; 1.
DR SMART; SM00542; FYRC; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00249; PHD; 4.
DR SMART; SM00508; PostSET; 1.
DR SMART; SM00184; RING; 2.
DR SMART; SM00317; SET; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS0280; SET; 1.
KW Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
KW Nuclear protein; Developmental protein; Activator.
FT ZN_FING 1251 1334 PHD-TYPE 1.
FT ZN_FING 1335 1380 PHD-TYPE 2.
FT ZN_FING 1408 1469 PHD-TYPE 3.
FT ZN_FING 1708 1767 PHD-TYPE 4 (ATYPICAL).
FT ZN_FING 1768 1818 PHD-TYPE 5 (ATYPICAL).
FT DOMAIN 3701 3810 SET.
FT DOMAIN 28 41 POLY-ALA.
FT DOMAIN 66 71 POLY-ASP.
FT DOMAIN 160 164 POLY-ASP.
FT DOMAIN 173 182 POLY-ALA.
FT DOMAIN 221 228 POLY-GLN.
FT DOMAIN 243 251 POLY-ALA.
FT DOMAIN 253 258 POLY-THR.
FT DOMAIN 292 296 POLY-ALA.
FT DOMAIN 538 546 POLY-ASP.
FT DOMAIN 1072 1075 POLY-GLU.
FT DOMAIN 2483 3271 GLN-RICH.
FT DOMAIN 3333 3339 POLY-ASP.
SQ SEQUENCE 3828 AA; 413721 MW; 32059CF303A3C504 CRC64;

Query Match 71.9%; Score 41; DB 1; Length 3828;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10

DB :|||:||||

618 KPKPKNYFGL 627

RESULT 13

TKN4_PSEGU

ID TKN4_PSEGU STANDARD; PRT; 11 AA.

AC P42989;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE SUBSTANCE P-LIKE PEPTIDE I (PG-SPI).

OS Pseudophryne guentheri (Frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoides; Myobatrachidae;

OC Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP SEQUENCE.

RC TISSUE=SKIN;

RX MEDLINE-90287814; PubMed-2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of

the Australian frog *Pseudophryne guentheri*."

RL Peptides 11:299-304(1990).

CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

CC MUSCLES.

CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR; E60409; E60409.

DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 0.14;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 :|:|:|:|:|
 Db 1 QPNPDEFFGL 10

RESULT 14

TKN5_PSEGU STANDARD; PRT; 11 AA.
 AC P42990;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P-LIKE PEPTIDE II (PG-SPII).
 OS Pseudophryne guntheri (Frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoldea; Myobatrachidae;
 CC Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.

RC TISSUE-Skin;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.

-!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR: F60409; F60409.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 0.14;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 :|:|:|:|:|
 Db 1 QPNPNEFFGL 10

RESULT 15

TKN1_KASMA STANDARD; PRT; 12 AA.
 ID TKN1_KASMA
 AC P08613;
 DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYLAMBATES KASSININ (GLU(2)-PRO(5) KASSININ).
 OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hyperoliidae;
 CC Kassina.
 OX NCBI_TaxID=8414;
 RN [1]
 RP SEQUENCE.
 RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
 RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
 RT hylambatin, in the skin of the African rhacophorid frog hylambates
 RT maculatus.";
 RL Biomed. Res. 2:613-617(1981).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: S10059; S10059.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 12;
 Best Local Similarity 77.8%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKPQOFFGL 10
 :|:|:|:|:|
 Db 3 RPKPQOFFGL 11

Search completed: March 15, 2002, 14:32:20
 Job time: 549 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:30:59 ; Search time 63.84 Seconds
(without alignments)
18.330 Million cell updates/sec

Title: US-09-988-792-12
Perfect score: 20
Sequence: 1 XPXPXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_prodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	70.0	9	2 Q99193	Q99193 pseudomonas
2	14	70.0	9	11 Q9QWT0	Q9QWT0 mus musculus
3	14	70.0	10	10 P81898	P81898 prunus dulc
4	14	70.0	10	11 Q9QVJ7	Q9QVJ7 mus sp. mep
5	14	70.0	11	4 Q9HCN5	Q9HCN5 homo sapien
6	14	70.0	12	10 P82441	P82441 nicotiana t
7	14	70.0	12	12 Q65027	Q65027 avian myelo
8	14	70.0	14	2 P81715	P81715 streptomyc
9	14	70.0	14	8 Q9TEN3	Q9TEN3 anas gracil
10	14	70.0	14	8 Q9TEN1	Q9TEN1 anas castan
11	14	70.0	15	3 Q9UR63	Q9UR63 emerice
12	14	70.0	15	4 Q9UCJ8	Q9UCJ8 homo sapien
13	14	70.0	15	4 Q00604	Q00604 homo sapien
14	14	70.0	15	4 Q9BXX4	Q9BXX4 homo sapien
15	14	70.0	15	11 Q9QV72	Q9QV72 mus sp. int
16	14	70.0	16	1 Q9UWJ4	Q9UWJ4 pyrococcus
17	14	70.0	16	3 Q9UR86	Q9UR86 candida par
18	14	70.0	16	4 Q9UQ54	Q9UQ54 homo sapien
19	14	70.0	16	4 Q9UC52	Q9UC52 homo sapien

20	14	70.0	16	6 Q77491	Q77491 nycticebus
21	14	70.0	16	6 Q9TRR1	Q9TRR1 oryctolagus
22	14	70.0	17	2 Q9R5J3	Q9R5J3 mycoplasma
23	14	70.0	17	4 Q9UC23	Q9UC23 homo sapien
24	14	70.0	17	4 Q9HB76	Q9HB76 homo sapien
25	14	70.0	17	6 Q9TR78	Q9TR78 didelphis m
26	14	70.0	18	6 Q9TR74	Q9TR74 bos taurus
27	14	70.0	19	3 Q9UR87	Q9UR87 candida par
28	14	70.0	19	4 Q9UQG7	Q9UQG7 homo sapien
29	14	70.0	19	6 Q9TRH3	Q9TRH3 sus scrofa
30	14	70.0	19	8 Q9XNQ7	Q9XNQ7 boophilus m
31	14	70.0	19	11 Q06028	Q06028 mus musculus
32	14	70.0	19	11 Q9QUY4	Q9QUY4 rattus sp.
33	14	70.0	19	13 Q9DFN3	Q9DFN3 gillichthys
34	14	70.0	20	2 Q52918	Q52918 rhizobium m
35	14	70.0	20	2 Q9RLP2	Q9RLP2 neisseria g
36	14	70.0	20	2 Q9R5R7	Q9R5R7 mycobacteri
37	14	70.0	20	2 Q9R4Z4	Q9R4Z4 proteus mir
38	14	70.0	20	2 Q9R4S0	Q9R4S0 mycobacteri
39	14	70.0	20	3 Q9UR76	Q9UR76 candida alb
40	14	70.0	20	4 Q9UM18	Q9UM18 homo sapien
41	14	70.0	20	6 Q28079	Q28079 bos taurus
42	14	70.0	20	10 Q41179	Q41179 chlamydomon
43	14	70.0	20	10 P82799	P82799 spinacia ol
44	14	70.0	20	11 Q9QW31	Q9QW31 rattus sp.
45	14	70.0	20	12 Q65710	Q65710 berne virus

ALIGNMENTS

RESULT 1
Q99193 PRELIMINARY; PRT; 9 AA.
AC Q99193;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)
DE HYPOTHETICAL PROTEIN IN RPOB 3'REGION (FRAGMENT).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RA Borodin A.M., Danilkovich A.V., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;
RL Dokl. Biochem. 302:1261-1265(1988).
DR EMBL; X15849; CAA33847.1;
KW Hypothetical protein.
FT NON_TER 9
SQ SEQUENCE 9 AA; 852 MW; 5B4167776DC76727 CRC64;

Query Match 70.0%; Score 14; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
Db 4 PAP 6

RESULT 2
Q9QWT0 PRELIMINARY; PRT; 9 AA.
ID Q9QWT0
AC Q9QWT0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PROTEINASE 3 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129 D3;
 RA Lutz P.G., Moog-Lutz C., Houzel-Charavel A., Cayre Y.E.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBB databases.
 DR EMBL; AJ007030; CAA07429.1;
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 937 MW; C91E75A77B45B87D CRC64;

Query Match 70.0%; Score 14; DB 11; Length 9;
 Best Local Similarity 66.7%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 6 PSP 8

RESULT 3

P81898
 ID P81898 PRELIMINARY; PRT; 10 AA.
 AC P81898;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE PEPTIDE-N4-(N-ACETYL-BETA-GLUCOSAMINYL)ASPARAGINE AMIDASE A, SMALL
 DE CHAIN (SUBUNIT B) (EC 3.5.1.52) (ENGASE A) (GLICOPEPTIDE N-
 DE GLYCOSIDASE) (N-GLUCANASE) (FRAGMENT).
 OS Prunus dulcis (Almond) (Prunus amygdalus).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Prunus.
 OX NCBI_TaxID=3755;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RX PubMed=9523720;
 RA "Altmann F., Paschinger K., Dalik T., Vorauer K.;
 RT "Characterisation of peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine
 RT amidase A and its N-glycans.";
 RL Eur. J. Biochem. 252:118-123(1998).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
 CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
 CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
 CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
 CC CONTAINING AN ASPARTIC RESIDUE.
 CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN
 CC -1- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
 CC DEGLYCOSYLATION.
 CC -1- MASS SPECTROMETRY: MW=21247; METHOD=MALDI-MS.
 KW Hydrolase; Glycoprotein.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1149 MW; 863278CAA1E73771 CRC64;

Query Match 70.0%; Score 14; DB 10; Length 10;
 Best Local Similarity 66.7%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 2 PTP 4

RESULT 4

Q9QVJ7
 ID Q9QVJ7 PRELIMINARY; PRT; 10 AA.
 AC Q9QVJ7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE MEPRIN-B.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373354; PubMed=1894622;
 RA Kounnas M.Z., Wolz R.L., Gorbea C.M., Bond J.S.;
 RT "Meprin-A and -B Cell surface endopeptidases of the mouse kidney.";
 RL J. Biol. Chem. 266:17350-17357(1991).
 SQ SEQUENCE 10 AA; 1031 MW; DAFBDEC9C87B076D CRC64;

Query Match 70.0%; Score 14; DB 11; Length 10;
 Best Local Similarity 66.7%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 2 PAP 4

RESULT 5

Q9HCN5
 ID Q9HCN5 PRELIMINARY; PRT; 11 AA.
 AC Q9HCN5;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE PLATELET GLYCOPROTEIN VI (FRAGMENT).
 GN GPVI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11027634;
 RA Ezumi Y., Uchiyama T., Takayama H.;
 RT "Molecular cloning, genomic structure, chromosomal localization, and
 RT alternative splice forms of the platelet collagen receptor
 RT glycoprotein VI.";
 RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
 DR EMBL; AB043943; BAB12248.1;
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1166 MW; 8D7839FE2DC1B775 CRC64;

Query Match 70.0%; Score 14; DB 4; Length 11;
 Best Local Similarity 66.7%; Pred. No. 4.8e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 3 PSP 5

RESULT 6

P82441
 ID P82441 PRELIMINARY; PRT; 12 AA.
 AC P82441;
 DT 01-JUN-2000 (TREMBlrel. 14, Created)
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE 26 KDA CELL WALL PROTEIN (FRAGMENT).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.

RC STRAIN=CV. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture."
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;
 Query Match 70.0%; Score 14; DB 10; Length 12;
 Best Local Similarity 66.7%; Pred. No. 5.1e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PXP 4
 DB 3 PAP 5
 RESULT 7
 ID Q65027 PRELIMINARY; PRT; 12 AA.
 AC Q65027;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE 5' END V-MYB GENE PRODUCT (FRAGMENT).
 OS Avian myeloblastosis virus.
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=11866;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B;
 RX MEDLINE=92391109; PubMed=1519362;
 RA Bartunek P., Kozmik Z., Dvorak M.;
 RT "Cloning and nucleotide sequence of the 5' part of v-myb cDNA."
 RL Virology 190:882-883(1992).
 DR EMBL: X51496; CAA35864.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1230 MW; 850C5E7D672D5BE CRC64;
 Query Match 70.0%; Score 14; DB 12; Length 12;
 Best Local Similarity 66.7%; Pred. No. 5.1e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PXP 4
 DB 8 PAP 10
 RESULT 8
 ID P81715 PRELIMINARY; PRT; 14 AA.
 AC P81715;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE LEUPEPTIN-INACTIVATING ENZYME (EC 3.4.24.-) (LIE) (FRAGMENT).
 OS Streptomyces exfoliatus (Streptomyces hydroganus).
 DE Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1905;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=SMF13;
 RX PubMed=9531495;
 RA Kim I.S., Kim Y.B., Lee K.J.;
 RT "Characterization of the leupeptin-inactivating enzyme from
 RT Streptomyces exfoliatus SMF13 which produces leupeptin.";

RL Biochem. J. 331:539-545(1998).
 CC -!- FUNCTION: A LEUCINE-SPECIFIC METALLOPROTEASE THAT PLAYS A ROLE IN
 CC CONTROLLING THE AMOUNT OF LEUPEPTIN DURING COLONY DEVELOPMENT.
 CC OPTIMUM PH IS 9.0-AND TEMPERATURE IS 40 DEGREES CELSIUS.
 CC -!- FUNCTION: DEGRADES LEUPEPTIN INTO THREE COMPONENTS, ACETYL-
 CC LEUCINE, LEUCINE AND ARGININAL.
 CC -!- CATALYTIC ACTIVITY: HAS A STRICT PREFERENCE FOR LEUCINE AT THE P1
 CC SITE.
 CC -!- ENZYME REGULATION: ACTIVITY IS INHIBITED BY METALLOPROTEASE
 CC INHIBITORS AND ACTIVATED BY MG2+ AND CA2+.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 KW Hydrolase; Metalloprotease.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1373 MW; 14D627940C973260 CRC64;
 Query Match 70.0%; Score 14; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 5.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PXP 4
 DB 2 PTP 4
 RESULT 9
 ID Q9TEN3 PRELIMINARY; PRT; 14 AA.
 AC Q9TEN3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE ATPASE 8 (FRAGMENT).
 OS Anas gracilis (grey teal).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=45630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kennedy M., Spencer H.G.;
 RT "Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
 RL Auk 0:0-0(2000).
 DR EMBL: AF173493; AAD51050.1; -.
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;
 Query Match 70.0%; Score 14; DB 8; Length 14
 Best Local Similarity 66.7%; Pred. No. 5.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PXP 4
 DB 6 PTP 8
 RESULT 10
 ID Q9TEN1 PRELIMINARY; PRT; 14 AA.
 AC Q9TEN1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE ATPASE 8 (FRAGMENT).
 OS Anas castanea (chestnut teal).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=45631;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kennedy M., Spencer H.G.;
 RT "Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
 RL Auk 0:0-0(2000).
 DR EMBL; AF173494; AAD51052.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;

Query Match
 Best Local Similarity 70.0%; Score 14; DB 8; Length 14;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 Db 6 PTP 8

RESULT 11
 Q9UR63 PRELIMINARY; PRT; 15 AA.
 AC Q9UR63;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE BETA-D-FRUCTOPURANOSIDE FRUCTOHYDROLASE 60 KDA HIGH MOLECULAR WEIGHT
 DE ISOFORM (EC 3.2.1.26) (FRAGMENT).
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Peizizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96409246; PubMed=8814228;
 RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;
 RT "Purification and partial characterization of the high and low
 RT molecular weight form (S- and F-form) of invertase secreted by
 RT Aspergillus nidulans";
 RT Biochim. Biophys. Acta 1296:207-218(1996).
 SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match
 Best Local Similarity 70.0%; Score 14; DB 3; Length 15;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 Db 8 PAP 10

RESULT 12
 Q9UCJ8 PRELIMINARY; PRT; 15 AA.
 AC Q9UCJ8;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE TYPE IV PROCOLLAGENASE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93125366; PubMed=1480041;
 RA Stetler-Stevenson W.G., Kruttsch H.C., Liotta L.A.;
 RT "TMP-2: Identification and characterization of a new member of the
 RT metalloproteinase inhibitor family";
 RL Matrix Suppl. 1:299-306(1992).
 SQ SEQUENCE 15 AA; 1537 MW; D5DA1AAA9C32276C CRC64;

Query Match
 Best Local Similarity 70.0%; Score 14; DB 4; Length 15;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 Db 2 PSP 4

RESULT 13
 O00604 PRELIMINARY; PRT; 15 AA.
 AC O00604;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE TYPE I COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).
 GN COL1A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96336021; PubMed=8757037;
 RA Meyer S.A., Rubin B.S., Starman B.J., Byers P.H.;
 RT "Spontaneous multivessel cervical artery dissection in a patient with
 RT a substitution of alanine for glycine (G13A) in the alpha 1 (I) chain
 RT of type I collagen";
 RL Neurology 47:552-556(1996).
 DR EMBL; S83315; AAB50780.2; -.
 KW Collagen.
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1413 MW; 4CA8D720AAF780FC CRC64;

Query Match
 Best Local Similarity 70.0%; Score 14; DB 4; Length 15;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 Db 9 PAP 11

RESULT 14
 Q9BXX4 PRELIMINARY; PRT; 15 AA.
 AC Q9BXX4;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE TRANSCRIPTION FACTOR PAX 5 (FRAGMENT).
 GN PAX5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hirabayashi Y., Rahman M., Sasaki T.;
 RT "Identification of a novel repressor element in the 5'UTR of human
 RT BSAP/Pax5A";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF268279; AAK25737.1; -.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;

Query Match
 Best Local Similarity 70.0%; Score 14; DB 4; Length 15;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 8 PTP 10

RESULT 15

Q9QV72

ID Q9QV72 PRELIMINARY; PRT; 15 AA.

AC Q9QV72;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE INTERFERON-ACTIVATED ANTIMICROBIAL PROTEIN (FRAGMENT).

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10095;

RN [1]

RP SEQUENCE.

RX MEDLINE=93293329; PubMed=8514411;

RA Hiemstra P.S., Eisenhauer P.B., Harwig S.S., van den Barselaar M.T.,

van Furth R., Lehrer R.I.;

RT "Antimicrobial proteins of murine macrophages.";

RL Infect. Immun. 61:3038-3046(1993).

SQ SEQUENCE 15 AA; 1470 MW; 8A5C937D823C90AE CRC64;

Query Match

Best Local Similarity 70.0%; Score 14; DB 11; Length 15;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 9 PAP 11

Search completed: March 15, 2002, 14:30:59

Job time: 578 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:32:19 ; Search time 20.4 Seconds
(without alignments)
14.378 Million cell updates/sec

Title: US-09-988-792-12
Perfect score: 20
Sequence: 1 XPXPXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	70.0	8	1 RS7_MYCIT	P33564 mycobacteri
2	14	70.0	10	1 TMOF_AEDAE	P19425 aedes aegyp
3	14	70.0	11	1 TKNA_RANCA	P22888 rana catesb
4	14	70.0	13	1 GER1_HORVU	P28525 hordeum vul
5	14	70.0	13	1 GER2_HORVU	P28526 hordeum vul
6	14	70.0	14	1 UHA1_CANFA	P99503 canis fami
7	14	70.0	15	1 CBPB_PROAT	P19628 protoperus
8	14	70.0	15	1 URE2_MORMO	P17338 morganella
9	14	70.0	16	1 FOR1_MYRGU	P81438 myrmecia gu
10	14	70.0	16	1 FOR2_MYRGU	P81437 myrmecia gu
11	14	70.0	16	1 H5_COTJA	P18638 coturnix co
12	14	70.0	16	1 OD02_BOVIN	P11179 bos taurus
13	14	70.0	17	1 A45K_MYCBO	P80069 mycobacteri
14	14	70.0	19	1 ATPB_CANFA	P99504 canis fami
15	14	70.0	19	1 ITHA_PERAM	P19986 periplaneta
16	14	70.0	20	1 PYRR_PYRAP	P37362 pyrrhocoris
17	14	70.0	21	1 LPRM_CORDI	P21232 corynebacte
18	14	70.0	24	1 HEMT_LINRE	P23543 lingula ree
19	14	70.0	24	1 HEMU_LINRE	P23544 lingula ree
20	14	70.0	25	1 PER_COPMA	P28315 coprinus ma
21	14	70.0	26	1 TPO_PIG	P42706 sus scrofa
22	14	70.0	27	1 DCUP_RHOSE	P32920 rhodobacter
23	14	70.0	27	1 IPPD_MOUSE	Q60829 mus musculu
24	14	70.0	28	1 GRP_ALIMI	P31886 alligator m
25	14	70.0	28	1 PHYB_ASFFI	P81440 aspergillus
26	14	70.0	30	1 RNP_ODOVI	P19640 odocoileus
27	14	70.0	32	1 ATP7_SPIOL	P80088 spinacia ol
28	14	70.0	32	1 FF21_SALEN	P55224 salmonella
29	14	70.0	32	1 YTK3_ILTVT	P23985 infectious
30	14	70.0	34	1 RNL1_PIG	P15466 sus scrofa
31	14	70.0	34	1 TXF5_BRASM	P49266 brachypelma
32	14	70.0	35	1 PH11_MYTCA	P35422 mytilus cal
33	14	70.0	36	1 IAA_STRAU	P04082 streptomyce

34	14	70.0	36	1 NLTP_PINPI	P26912 pinus pinea
35	14	70.0	36	1 PMY_PETMA	P80024 petromyzon
36	14	70.0	36	1 PSAH_PEA	P20121 pisum sativ
37	14	70.0	38	1 CRS3_NOTGO	P15534 nototodar
38	14	70.0	38	1 H5_COLLI	P02260 columba liv
39	14	70.0	38	1 PSBT_WHEAT	P37260 triticum ae
40	14	70.0	38	1 Y232_TREPA	O83260 treponema p
41	14	70.0	39	1 PDA3_PAPHA	P81246 papio hamad
42	14	70.0	40	1 Y041_TREPA	O83082 treponema p
43	14	70.0	41	1 LAMA_EMENI	P38095 emerice
44	14	70.0	42	1 NGF_VIPLE	P25428 vipera lebe
45	14	70.0	42	1 V042_ASFB7	P23168 african swi

ALIGNMENTS

```
RESULT 1
RS7_MYCIT
ID RS7_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S7 (FRAGMENT).
GN RPSG.
OS Mycobacterium intracellulare.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93197130; PubMed=8451173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -!- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
CC 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L08171; AAA25376.1;
CC PIR; S35538; S35538.
CC InterPro; IPR000235; RIBOSOMAL_S7.
CC ProSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT INIT_MET 0 BY SIMILARITY.
FT NIT_TER 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;
```

Query Match 70.0%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 9.9e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	PXP	4
DB	5	PAP	7
RESULT 2			
TMOF_AEDAE		STANDARD;	PRT; 10 AA.
ID TMOF_AEDAE			
AC P19425;			
DT 01-NOV-1990 (Rel. 16, Created)			

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE TRYPsin-MODULATING OOSTATIC FACTOR (TMOF) (OOSH).
 OS Aedes aegypti (yellow fever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 OC Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RN SEQUENCE.
 RP STRAIN=VERO BEACH; TISSUE=Ovary;
 RC MEDLINE=90367888; PubMed=2394318;
 RX Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RA "Mosquito oostatic factor: a novel decapetide modulating
 RT trypsin-like enzyme biosynthesis in the midgut.";
 RL FASEB J. 4:3015-3020(1990).
 RN [2]
 RN SEQUENCE.
 RP STRAIN=VERO BEACH; TISSUE=Ovary;
 RC MEDLINE=93357794; PubMed=8353526;
 RX Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RA "Mass spectrometry and characterization of Aedes aegypti trypsin
 RT modulating oostatic factor (TMOF) and its analogs.";
 RL Insect Biochem. Mol. Biol. 23:703-712(1993).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
 CC DEVELOPMENT.
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
 CC 36 HRS AND STOPS AT 56 HRS.
 CC PIR: A36454; A36454.
 DR Hormone.
 KW DOMAIN 3 10 POLY-PRO.
 FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
 SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;
 Query Match 70.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 5.5e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PXP 4
 Db 3 PAP 5
 RESULT 3
 TKNA_RANCA
 ID TKNA_RANCA STANDARD; PRT; 11 AA.
 AC P22688;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RANATACHYKININ A (RTK A).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RN SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 RL brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RN SEQUENCE.
 RP TISSUE=Intestine;
 RC MEDLINE=94023216; PubMed=8210506;
 RX Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and

RT Intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: JE0426; JE0426.
 DR PIR: A61033; A61033.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;
 Query Match 70.0%; Score 14; DB 1; Length 11;
 Best Local Similarity 66.7%; Pred. No. 6e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PXP 4
 Db 2 PSP 4

RESULT 4
 GERL_HORVU
 ID GERL_HORVU STANDARD; PRT; 13 AA.
 AC P28525;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GERMIN GSI (FRAGMENT).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RN SEQUENCE.
 RC STRAIN=CV. CM 72; TISSUE=Root;
 RA Hukman W.J., Tao H.P., Tanaka C.K.;
 RT "Germin-like polypeptides increase in barley roots during salt
 RT stress.";
 RL Plant Physiol. 97:366-374(1991).
 CC -!- FUNCTION: MAY PLAY A ROLE IN ALTERING THE PROPERTIES OF CELL
 CC WALLS DURING GERMINATIVE GROWTH.
 CC -!- SUBUNIT: OLIGOMER (BELIEVED TO BE A PENTAMER BUT PROBABLY
 CC HEXAMER) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.
 CC -!- TISSUE SPECIFICITY: ROOTS AND COLEOPTILE IN ROOTS. PRESENT IN
 CC THE MATURE REGION, BUT NOT IN THE TIP. NOT DETECTED IN LEAVES.
 CC -!- INDUCTION: INCREASED BY SALT STRESS IN ROOTS AND DECREASED BY SALT
 CC STRESS IN COLEOPTILE.
 CC -!- PTM: GLYCOSYLATED.
 CC -!- SIMILARITY: BELONGS TO THE GERMIN FAMILY.
 DR InterPro: IPR001929; Germin.
 DR PROSITE: PS00725; GERMIN; PARTIAL.
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.
 FT UNSURE 10 10
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1470 MW; 43FB588AA3B7B6D7 CRC64;
 Query Match 70.0%; Score 14; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 6.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PXP 4
 Db 1 1

Db 3 PSP 5

RESULT 5

GER2_HORVU STANDARD; PRT; 13 AA.
 AC P28526;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GERMIN GS2 (FRAGMENT).
 OS Hordeum vulgare (barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-CV. CM 72; TISSUE=Root;
 RA Hukman W.J., Tao H.P., Tanaka C.K.;
 RT "Germin-like polypeptides increase in barley roots during salt stress."
 RL Plant Physiol. 97:366-374(1991).
 CC -!- FUNCTION: MAY PLAY A ROLE IN ALTERING THE PROPERTIES OF CELL WALLS DURING GERMINATIVE GROWTH.
 CC -!- SUBUNIT: OLIGOMER (BELIEVED TO BE A PENTAMER BUT PROBABLY HEXAMER) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.
 CC -!- TISSUE SPECIFICITY: ROOTS AND COLEOPTILE. IN ROOTS, PRESENT IN THE MATURE REGION, BUT NOT IN THE TIP. NOT DETECTED IN LEAVES.
 CC -!- INDUCTION: INCREASED BY SALT STRESS IN ROOTS AND DECREASED BY SALT STRESS IN COLEOPTILE.
 CC -!- PTM: GLYCOSYLATED.
 CC -!- SIMILARITY: BELONGS TO THE GERMIN FAMILY.
 DR InterPro: IPR001929; Germin.
 DR PROSITE: PS00725; GERMIN; PARTIAL.
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.
 FT UNSURE 10 10
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;

Query Match

Best Local Similarity 70.0%; Score 14; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 6.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 3 PSP 5

RESULT 6

UHAL_CANFA STANDARD; PRT; 14 AA.
 AC P99503;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT 11) (FRAGMENT).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2D-PAGE and the two-dimensional gel electrophoresis database of dog heart proteins."
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.3, ITS MW IS: 19.6 KDA.

DR HSC-2DPAGE; P99503; DOG.

FT NON_TER 14 14

SQ SEQUENCE 14 AA; 1149 MW; 3D9238888D8668C7 CRC64;

Query Match

Best Local Similarity 70.0%; Score 14; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 7.3e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 7 PAP 9

RESULT 7

CBPB_PROAT STANDARD; PRT; 15 AA.
 AC P19628;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CARBOXYPEPTIDASE B (EC 3.4.17.2) (FRAGMENT).
 OS Protopterus aethiopicus (Marbled lungfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Dipnoi; Lepidosireniformes; Protopterae; Protopterus.
 OX NCBI_TaxID=7886;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=73025047; PubMed=5079891;
 RA Reeck G.R., Neurath H.;
 RT "Isolation and characterization of pancreatic procarboxypeptidase B and carboxypeptidase B of the African lungfish."
 RL Biochemistry 11:3947-3955(1972).
 CC -!- CATALYTIC ACTIVITY: PEPTIDYL-L-LYSINE/ARGININE + H(2)O = PEPTIDE + L-LYSINE/ARGININE.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14; ALSO KNOWN AS THE ZINC CARBOXYPEPTIDASE FAMILY.
 CC PIR: A26212; A26212.
 DR MEROPS: M14.003;
 DR InterPro: IPR000834; Zn_carboxpept.
 DR PROSITE: PS00132; CARBOXYPEPT_ZN_1; PARTIAL.
 DR PROSITE: PS00133; CARBOXYPEPT_ZN_2; PARTIAL.
 KW Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Zymogen.
 FT PROPEP 1 >15
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1749 MW; 124C910D937BED65 CRC64;

Query Match

Best Local Similarity 70.0%; Score 14; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 7.7e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 2 PTP 4

RESULT 8

URE2_MORMO STANDARD; PRT; 15 AA.
 AC P17338;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE UREASE BETA SUBUNIT (EC 3.5.1.15) (15 KDA SUBUNIT) (UREA AMIDOHYDROLASE) (FRAGMENT).
 GN UREB.
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Morganella.
 OX NCBI_TaxID=582;
 RN [1]

```

RP SEQUENCE
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RL isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -|- CATALYTIC ACTIVITY: UREA + H(2)O -> CO(2) + 2 NH(3).
CC -|- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -|- SIMILARITY: TO OTHER UREASES BETA SUBUNITS.
DR PIR; B35389; B35389.
KW Hydrolase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Query Match 70.0%; Score 14; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.7e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 6 PTP 8

RESULT 9
FOR1_MYRGU
ID FOR1_MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FORMACIN 1.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Formicidae; Myrmecilinae; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RX MEDLINE=98165787; PubMed=9497332;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible
RT O-glycosylated proline-rich antibacterial peptides.";
RL J. Biol. Chem. 273:6139-6143(1998).
CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI
CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
CC BACTERIA.
CC -|- INDUCTION: UPON BACTERIAL CHALLENGE.
CC -|- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
CC -|- SIMILARITY: TO DROSOPHILA DROSOCIN.
CC Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
KW CARBOHYD 11 11 O-LINKED (GALNAC. .).
FT CARBOHYD 11 11
SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 70.0%; Score 14; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 10 PTP 12

RESULT 11
H5_COTJA
ID H5_COTJA STANDARD; PRT; 16 AA.
AC P18638;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HISTONE H5 (FRAGMENT).
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277939; PubMed=962913;
RA Sellyg V., Roy C., Dove M., Yaguchi M.;
RT "Species variability of N-terminal sequence of avian erythrocyte-
RT specific histone H5.";
RL Biochem. Biophys. Res. Commun. 71:196-202(1976).
CC -|- FUNCTION: HISTONE H5 PERFORMS THE SAME FUNCTION AS H1, BEING
CC NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER
CC ORDER STRUCTURES, AND REPLACES HISTONE H1 IN CERTAIN CELLS.
CC -|- SUBCELLULAR LOCATION: NUCLEAR.
CC -|- TISSUE SPECIFICITY: ERYTHROID CELLS.
CC -|- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
KW Chromosomal protein; Nuclear protein; DNA-binding; DNA condensation.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1665 MW; DB528219B3074D3C CRC64;

Query Match 70.0%; Score 14; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 8 PAP 10

RESULT 10
FOR2_MYRGU
ID FOR2_MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

```

```

DE FORMACIN 2.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Formicidae; Myrmecilinae; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE=Hemolymph;
RX MEDLINE=98165787; PubMed=9497332;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible
RT O-glycosylated proline-rich antibacterial peptides.";
RL J. Biol. Chem. 273:6139-6143(1998).
CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI
CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
CC BACTERIA.
CC -|- INDUCTION: UPON BACTERIAL CHALLENGE.
CC -|- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
CC -|- SIMILARITY: TO DROSOPHILA DROSOCIN.
CC Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
KW CARBOHYD 11 11 O-LINKED (GALNAC. .).
FT CARBOHYD 11 11
SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 70.0%; Score 14; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 10 PTP 12

RESULT 11
H5_COTJA
ID H5_COTJA STANDARD; PRT; 16 AA.
AC P18638;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HISTONE H5 (FRAGMENT).
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277939; PubMed=962913;
RA Sellyg V., Roy C., Dove M., Yaguchi M.;
RT "Species variability of N-terminal sequence of avian erythrocyte-
RT specific histone H5.";
RL Biochem. Biophys. Res. Commun. 71:196-202(1976).
CC -|- FUNCTION: HISTONE H5 PERFORMS THE SAME FUNCTION AS H1, BEING
CC NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER
CC ORDER STRUCTURES, AND REPLACES HISTONE H1 IN CERTAIN CELLS.
CC -|- SUBCELLULAR LOCATION: NUCLEAR.
CC -|- TISSUE SPECIFICITY: ERYTHROID CELLS.
CC -|- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
KW Chromosomal protein; Nuclear protein; DNA-binding; DNA condensation.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1665 MW; DB528219B3074D3C CRC64;

Query Match 70.0%; Score 14; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 8 PAP 10

RESULT 10
FOR2_MYRGU
ID FOR2_MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

```

```

RESULT 12
ODO2_BOVIN STANDARD; PRT; 16 AA.
AC P11179;
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE
DE DEHYDROGENASE COMPLEX (EC 2.3.1.61) (E2) (FRAGMENT).
GN DUST.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC MEDLINE=88005143; PubMed=3115829;
RA Bradford A.P., Aitken A., Beg F., Cook K.G., Yeaman S.J.;
RT "Amino acid sequence surrounding the lipoic acid cofactor of bovine
RL kidney 2-oxoglutarate dehydrogenase complex.";
RL FEBS Lett. 222:211-214(1987).
CC -1- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE
CC OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-COA & CO(2). IT
CC CONTAINS MULTIPLE COPIES OF 3 ENZYMIC COMPONENTS: 2-OXOGLUTARATE
CC DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) &
CC LIPONAMIDE DEHYDROGENASE (E3).
CC -1- CATALYTIC ACTIVITY: SUCCINYL-COA + DIHYDROLIPOAMIDE = COA +
CC S-SUCCINYLDIHYDROLIPOAMIDE.
CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
CC COFACTOR.
CC -1- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -1- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
DR PIR; S00123; S00123.
DR InterPro; IPR003016; Lipoyl.
DR PROSITE; PS00189; LIPOYL; PARTIAL.
KW Glycolysis; Transferrase; Acyltransferase; Lipoyl; Mitochondrion.
FT NON_TER 1 1
FT BINDING 5 5 LIPOYL.
FT NON_TER 16 16
FT SEQUENCE 16 AA; 1643 MW; E34CD29B86B3239D CRC64;

Query Match 70.0%; Score 14; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 11 PSP 13

RESULT 13
A45K_MYCBO STANDARD; PRT; 17 AA.
AC P80069;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 45/47 KDA ANTIGEN (FRAGMENT).
OS Mycobacterium bovis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / PARIS 1173 P2;

Query Match 70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 6 PSP 8

RX MEDLINE=93138802; PubMed=8423100;
RA Romain F., Laqueyrie A., Militzer P., Pescher P., Chav...t P.,
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;
RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen
RT complex, an immunodominant target for antibody response after
RT immunization with living bacteria.";
RL Infect. Immun. 61:742-750(1993).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.
DR PIR; A49237; A49237.
KW Antigen.
FT NON_TER 17 17
FT SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 70.0%; Score 14; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 4 PAP 6

RESULT 14
ATPB_CANFA STANDARD; PRT; 19 AA.
AC P99504;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL (EC 3.6.1.34) (FRAGMENT).
GN ATP5B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
DR HSC-2DPAGE; P99504; DOG.
DR InterPro; IPR000194; ATPase_alpha_beta.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolyase; ATP-binding;
KW Mitochondrion.
FT UNSURE 8 8
FT NON_TER 17 19
FT SEQUENCE 19 AA; 1871 MW; BB9C163FDC60BB42 CRC64;

Query Match 70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
DB 6 PSP 8
```

RESULT 15

ITHA_PERAM
 ID ITHA_PERAM STANDARD; PRT; 19 AA.
 AC P19986;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE TREHALASE INHIBITOR (FRAGMENT).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph; PubMed=2777784;
 RX MEDLINE=89380218; Yaguchi M., Downer R.G.H.;
 RA Hayakawa Y., Jahagirdar A.P., Yaguchi M., Downer R.G.H.;
 RT "Purification and characterization of trehalase inhibitor from
 hemolymph of the American cockroach, Periplaneta americana.";
 RL J. Biol. Chem. 264:16165-16169(1989).
 CC -!- FUNCTION: UNDER RESTING CONDITIONS, INHIBITS TREHALASE IN A
 DOSE-DEPENDENT MANNER.
 DR PIR; A34233; A34233.
 KW Glycoprotein.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2016 MW; A60C3A3397AF9A22 CRC64;

Query Match 70.0%; Score 14; DB 1; Length 19;
 Best Local Similarity 66.7%; Pred. No. 9.3e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 Db 3 PTP 5

Search completed: March 15, 2002, 14:32:20
 Job time: 549 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:23:48 ; Search time 34.92 Seconds
(without alignments)
17.451 Million cell updates/sec

Title: US-09-988-792-12
Perfect score: 20
Sequence: 1 XPXPXXXX 8
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	70.0	5	2 B60274	major protein anti
2	14	70.0	8	2 S21288	lectin - potato (f
3	14	70.0	9	2 S35338	ribosomal protein
4	14	70.0	10	2 B59272	peptide-N4-(N-acet
5	14	70.0	10	2 A36454	trypsin-modulating
6	14	70.0	11	2 A61033	ranatichykinin A -
7	14	70.0	12	2 S65409	histone H2B - huma
8	14	70.0	13	2 A60458	protocatechuete 3,
9	14	70.0	13	2 S36668	hypothetical prote
10	14	70.0	13	2 A40207	cell surface glyco
11	14	70.0	14	2 S48685	extension protein
12	14	70.0	15	2 B35389	urease (EC 3.5.1.5
13	14	70.0	15	2 PA0088	protein QF200051 -
14	14	70.0	15	2 A26212	carboxypeptidase B
15	14	70.0	15	2 S67975	apolipoprotein Cb2
16	14	70.0	16	2 S00123	dihydrolipoamide S
17	14	70.0	16	2 A42411	myosin light chain
18	14	70.0	16	2 B23692	transcription fact
19	14	70.0	17	2 A49237	45/47k antigen - M
20	14	70.0	17	2 S33609	extensin - maize (
21	14	70.0	17	2 A39111	Ig light chain - p
22	14	70.0	17	2 C49255	T-cell receptor be
23	14	70.0	17	2 B25348	UDPglucose-glyco
24	14	70.0	18	2 S65454	asparagillopepsin I
25	14	70.0	18	2 A61220	epsilon receptor m
26	14	70.0	18	2 I78841	thrombopoietin rec
27	14	70.0	19	2 S20289	cytochrome-c oxida
28	14	70.0	19	2 PC1251	testin II - rat (f
29	14	70.0	19	2 A34233	trehalase inhibito

30	14	70.0	19	2 D49404	T-cell receptor be
31	14	70.0	19	2 S25715	hypothetical prote
32	14	70.0	19	2 S12268	Oa-2 antigen - mou
33	14	70.0	20	2 S29817	cytochrome P450 2C
34	14	70.0	20	2 S3878	myosin light chain
35	14	70.0	20	2 S19240	histone H2B (clone
36	14	70.0	20	2 S59494	formate dehydrogen
37	14	70.0	20	2 S61281	probable L-histidi
38	14	70.0	20	2 C57789	gallbladder stone
39	14	70.0	20	2 B33290	histone H2B - huma
40	14	70.0	20	2 PH1341	Ig heavy chain DJ
41	14	70.0	20	2 PQ0537	arylhydroxamic aci
42	14	70.0	20	2 B35473	H-transferrin AT
43	14	70.0	20	2 S44465	pyrrolicorcin - Py
44	14	70.0	21	2 S38739	lipid transfer pro
45	14	70.0	21	2 F28027	protein P9 - curle

ALIGNMENTS

RESULT 1

B60274

major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)

C:Species: Mycobacterium tuberculosis

C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C:Accession: B60274

R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A:Title: Isolation and partial characterization of major protein antigens in the cult

A:Reference number: A60274; MUID:9109989

A:Accession: B60274

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <NAG>

Query Match 70.0%; Score 14; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PXP 4

Db 2 PAP 4

RESULT 2

S21288

lectin - potato (fragment)

C:Species: Solanum tuberosum (potato)

C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998

C:Accession: S21288

R:Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.

Biochem. J. 283, 813-821, 1992

A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characteriza

A:Reference number: S21288; MUID:92272683

A:Accession: S21288

A:Molecule type: protein

A:Residues: 1-8 <MIL>

A:Experimental source: var. Ulster Sceptre

C:Function:

A:Description: may be involved in defence mechanism of the plant

C:Keywords: hydroxyproline; lectin

Query Match 70.0%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PXP 4

Db 5 PSP 7

RESULT 3

S35538

ribosomal protein S7 - Mycobacterium intracellulare (fragment)

C:Species: Mycobacterium intracellulare

C>Date: 09-Dec-1993 #sequence_revision 14-Nov-1997 #text_change 13-Aug-1999

C:Accession: S35538

R:Nair, J.; Rouse, D.; Morris, S.

Nucleic Acids Res. 21, 1039, 1993

A:Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intracellulare

A:Reference number: S35537; MUID:93197130

A:Accession: S35538

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-9 <NAI>

A:Cross-references: EMBL:L08171; NID:g149994; PIDN:AAA25376.1; PID:g551901

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1993

C:Superfamily: Escherichia coli ribosomal protein S7

C:Keywords: protein biosynthesis; ribosome

Query Match

70.0%; Score 14; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

| |

Db 6 PAP 8

RESULT 4

B59272

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain

N:Alternate names: peptide N-glycosidase

C:Species: Prunus dulcis var. sativa (sweet almond)

C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000

C:Accession: B59272

R:Altman, F.; Paschinger, K.; Dalik, T.; Voraue, K.

Eur. J. Biochem. 252, 118-123, 1998

A:Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase

A:Reference number: A59272; MUID:98181894

A:Accession: B59272

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <ALT>

C:Keywords: hydrolase

Query Match

70.0%; Score 14; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.7e+02;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

| |

Db 2 PTP 4

RESULT 5

A36454

trypsin-modulating oostatic factor - yellow fever mosquito

C:Species: Aedes aegypti (yellow fever mosquito)

C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-May-1996

C:Accession: A36454; A61630

R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

FASEB J. 4, 3015-3020, 1990

A:Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi

A:Reference number: A36454; MUID:90367888

A:Accession: A36454

A:Molecule type: protein

A:Residues: 1-10 <BOR>

R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

Insect Biochem. Mol. Biol. 23, 703-712, 1993

A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost

A:Reference number: A61630; MUID:93357794

A:Accession: A61630

A:Molecule type: protein

A:Residues: 1-10 <BO2>

A>Note: none of the amino acids is modified

C:Function:

A:Description: Inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut

C:Keywords: hormone

Query Match

70.0%;

Best Local Similarity 66.7%; Pred. No. 7.7e+02;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

| |

Db 3 PAP 5

RESULT 6

A61033

ranatachykinin A - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C:Accession: A61033; JE0426

R:Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and i

A:Reference number: A61033

A:Accession: A61033

A:Molecule type: protein

A:Residues: 1-11 <KAN>

R:Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and i

A:Reference number: JE0426; MUID:91254337

A:Accession: JE0426

A:Molecule type: protein

A:Residues: 1-11 <KO2>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; neuropeptide

F.11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

70.0%;

Best Local Similarity 66.7%; Pred. No. 8.4e+02;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

| |

Db 2 PSP 4

RESULT 7

S65409

histone H2B - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S65409

R:Frohm, M.; Gunne, H.; Bergman, A.C.; Agerberth, B.; Bergman, T.; Liden, Eur. J. Biochem. 237, 86-92, 1996

A:Title: Biochemical and antibacterial analysis of human wound and blister fluid.

A:Reference number: S65409; MUID:96203912

A:Accession: S65409

A:Molecule type: protein

A:Residues: 1-12 <FRO>

C:Superfamily: histone H2B

C:Keywords: chromosomal protein; DNA binding; nucleosome core

Query Match

70.0%;

Best Local Similarity 66.7%; Pred. No. 9.1e+02;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 8 PAP 10

RESULT 8
A60458
protocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain GU2)
N:Alternate names: protocatechuate oxygenase
C:Species: Moraxella sp.
C>Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
C:Accession: A60458
R:Sterliades, R.; Pelmont, J.
Appl. Environ. Microbiol. 55, 340-347, 1989
A:Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a Moraxella sp.
A:Reference number: A60458; MUID:89245845
A:Accession: A60458
A:Molecule type: protein
A:Residues: 1-13 <STE>
A:Note: two forms P and G of the alpha subunit yielded identical amino terminal sequence
C:Keywords: iron; oxidoreductase

Query Match 70.0%; Score 14; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 7 PAP 9

RESULT 9
S36668
hypothetical protein l33 - Plectonema boryanum (fragment)
C:Species: Plectonema boryanum
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1999
C:Accession: S36668
R:Fujita, Y.; Matsumoto, H.; Takahashi, Y.; Matsubara, H.
submitted to the EMBL Data Library, August 1992
A:Description: Identification of the nifDK-like gene (ORF467) involved in the biosynthesis of iron
A:Reference number: S36668
A:Accession: S36668
A:Molecule type: DNA
A:Residues: 1-13 <FUJ>
A:Cross-references: EMBL:D12973; NID:g216810; PIDN:BAA02348.1; PID:dl002847; PID:g216811

Query Match 70.0%; Score 14; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 10 PXP 12

RESULT 10
A40207
cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C>Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 31-Dec-1993
C:Accession: A40207
R:Gao, E.N.; Shier, P.; Siu, C.H.
J. Biol. Chem. 267, 9409-9415, 1992
A:Title: Purification and partial characterization of a cell adhesion molecule (gp150) from Dictyostelium discoideum
A:Reference number: A40207; MUID:92250549
A:Accession: A40207
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <GAO>

C:Keywords: glycoprotein

Query Match 70.0%; Score 14; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 4 PTP 6

RESULT 11

S48685

extension protein - Streptomyces sp.

C:Species: Streptomyces sp.

C>Date: 28-Oct-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999

C:Accession: S48685

R:Fanuel, L.; Granier, B.; Wilkin, J.M.; Bellefroid-Bourguignon, C.; Joris, B.; Knowlton, J.

FEBS Lett. 351, 49-52, 1994

A:Title: The precursor of the Streptomyces R61 DD-peptidase containing a C-terminal extension protein

A:Reference number: S48685; MUID:94357278

A:Accession: S48685

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <FAN>

A:Note: the source is designated as Streptomyces R61

Query Match 70.0%; Score 14; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 9 PAP 11

RESULT 12

B35389

urease (EC 3.5.1.5) 15K chain - Morganella morganii (fragment)

C:Species: Morganella morganii

C>Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993

C:Accession: B35389

R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J. Bacteriol. 172, 3073-3080, 1990

A:Title: Morganella morganii urease: purification, characterization, and isolation of the urease gene

A:Reference number: A35389; MUID:90264298

A:Accession: B35389

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <HUA>

C:Keywords: hydrolase

Query Match 70.0%; Score 14; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 6 PTP 8

RESULT 13

PA0088

protein QF200051 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C:Accession: PA0088

R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A:Reference number: PA0051
A:Accession: PA0088
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 70.0%; Score 14; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 11 PAP 13

RESULT 14

A26212

carboxypeptidase B (EC 3.4.17.2) precursor - marbled lungfish (fragment)

C:Species: Protopterus aethiopicus (marbled lungfish)

C:Date: 10-Sep-1987 #sequence_revision 10-Sep-1987 #text_change 28-Apr-1993

C:Accession: A26212

R:Reeck, G.R.; Neurath, H.

Biochemistry 11, 3947-3955, 1972

A:Title: Isolation and characterization of pancreatic procarboxypeptidase B and carboxypeptidase B

A:Reference number: A90363; MUID:73025047

A:Accession: A26212

A:Molecule type: protein

A:Residues: 1-15 <REE>

C:Keywords: hydrolase; metallo-carboxypeptidase

Query Match 70.0%; Score 14; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 2 PTP 4

RESULT 15

S67975

apolipoprotein Cb2 - goose (fragment)

C:Species: Anser anser (domestic goose)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C:Accession: S67975

R:Hermier, D.; Sellier, N.; Rousselot-Pailley, D.; Forgez, P.

Eur. J. Biochem. 234, 586-591, 1995

A:Title: Characterization of apolipoproteins B-100, AI and C from plasma lipoprotein in

A:Reference number: S67972; MUID:96128192

A:Accession: S67975

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <HER>

Query Match 70.0%; Score 14; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 10 PAP 12

Search completed: March 15, 2002, 14:23:49
Job time: 223 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:31:52 ; Search time 48.07 Seconds
(without alignments)
10.615 Million cell updates/sec

Title: US-09-988-792-12

Perfect score: 20

Sequence: 1 XPXPXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 302707 segs, 63781257 residues

Total number of hits satisfying chosen parameters: 302707

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending_Patents_AA_New:*
- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
 - 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
 - 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
 - 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
 - 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
 - 6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
 - 7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
 - 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	70.0	3	6	US-09-295-996A-31
2	14	70.0	3	6	US-09-296-113C-31
3	14	70.0	3	6	US-09-551-737C-34
4	14	70.0	4	6	US-09-825-561A-70
5	14	70.0	4	6	US-09-592-066A-46
6	14	70.0	4	6	US-09-290-376A-29
7	14	70.0	4	7	US-10-007-649-74
8	14	70.0	5	5	US-09-009-986-31
9	14	70.0	5	6	US-09-295-996A-11
10	14	70.0	5	6	US-09-295-996A-19
11	14	70.0	5	6	US-09-295-996A-27
12	14	70.0	5	6	US-09-295-996A-33
13	14	70.0	5	6	US-09-295-996A-46
14	14	70.0	5	6	US-09-295-996A-50
15	14	70.0	5	6	US-09-295-996A-51
16	14	70.0	5	6	US-09-295-996A-52
17	14	70.0	5	6	US-09-295-996A-54
18	14	70.0	5	6	US-09-295-996A-55
19	14	70.0	5	6	US-09-296-113C-11
20	14	70.0	5	6	US-09-296-113C-18
21	14	70.0	5	6	US-09-296-113C-27
22	14	70.0	5	6	US-09-296-113C-33
23	14	70.0	5	6	US-09-296-113C-46
24	14	70.0	5	6	US-09-296-113C-50
25	14	70.0	5	6	US-09-296-113C-51

26	14	70.0	5	6	US-09-296-113C-52
27	14	70.0	5	6	US-09-296-113C-54
28	14	70.0	5	6	US-09-296-113C-57
29	14	70.0	5	6	US-09-551-737C-14
30	14	70.0	5	6	US-09-551-737C-21
31	14	70.0	5	6	US-09-551-737C-30
32	14	70.0	5	6	US-09-551-737C-36
33	14	70.0	5	6	US-09-551-737C-49
34	14	70.0	5	6	US-09-551-737C-53
35	14	70.0	5	6	US-09-551-737C-54
36	14	70.0	5	6	US-09-551-737C-55
37	14	70.0	5	6	US-09-551-737C-57
38	14	70.0	5	6	US-09-551-737C-58
39	14	70.0	5	7	US-10-068-569-9
40	14	70.0	6	6	US-09-295-996A-12
41	14	70.0	6	6	US-09-897-188-5
42	14	70.0	6	6	US-09-296-113C-12
43	14	70.0	6	6	US-09-976-736-55
44	14	70.0	6	6	US-09-625-049A-41
45	14	70.0	6	6	US-09-625-049A-43

ALIGNMENTS

RESULT 1
US-09-295-996A-31
; Sequence 31, Application US/09295996A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Linderman, Russell J.
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UP-230
; CURRENT APPLICATION NUMBER: US/09/295,996A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996A-31

Query Match 70.0%; Score 14; DB 6; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Gaps 0;

OY 2 PXP 4
| |
Db 1 PAP 3

RESULT 2
US-09-296-113C-31
; Sequence 31, Application US/09296113C
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
; FILE REFERENCE: UP-224
; CURRENT APPLICATION NUMBER: US/09/296,113C
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-296-113C-31

Query Match 70.0%; Score 14; DB 6; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 1 PAP 3

RESULT 3
US-09-551-737C-34
; Sequence 34, Application US/09551737C
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Schlesinger, Yaagov
; APPLICANT: Nauwelaers, Sabine M. I.
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223C1
; CURRENT APPLICATION NUMBER: US/09/551,737C
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/295,846
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-551-737C-34

Query Match 70.0%; Score 14; DB 6; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 1 PAP 3

RESULT 4
US-09-825-561A-70
; Sequence 70, Application US/09825561A
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Novak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Domain linker motif; PAPP motif
US-09-825-561A-70

Query Match 70.0%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 1 PAP 3

RESULT 5
US-09-592-066A-46
; Sequence 46, Application US/09592066A
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Bjornvad, Mads Eskelund
; APPLICANT: Diers, Ivan
; TITLE OF INVENTION: Pectate lyase fusion for expression and secretion of polypepti
; FILE REFERENCE: 5863.204-US
; CURRENT APPLICATION NUMBER: US/09/592,066A
; CURRENT FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-592-066A-46

Query Match 70.0%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 2 PTP 4

RESULT 6
US-09-290-376A-29
; Sequence 29, Application US/09290376A
; GENERAL INFORMATION:
; APPLICANT: Wallner, Barbara P.
; TITLE OF INVENTION: Multivalent Compounds for Crosslinking, Targeting and Inhibiti
; FILE REFERENCE: I0248/7013/ERP/JAV
; CURRENT APPLICATION NUMBER: US/09/290,376A
; CURRENT FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/837,305
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 08/671,756
; PRIOR FILING DATE: 1996-06-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: (4)...(4)
; OTHER INFORMATION: xaa is any amino acid
US-09-290-376A-29

QY 2 PXP 4
| |

Db 1 PTP 3

RESULT 7

US-10-007-649-74

; Sequence 74, Application US/10007649
; GENERAL INFORMATION:
; APPLICANT: Turk, Benjamin
; APPLICANT: Cantley, Lewis
; TITLE OF INVENTION: Methods for Determining Protease Cleavage Site Motifs
; FILE REFERENCE: B0662/7044
; CURRENT APPLICATION NUMBER: US/10/007,649
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/246,815
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: (1)..(4)
; OTHER INFORMATION: Synthetic Peptide
US-10-007-649-74

Query Match 70.0%; Score 14; DB 7; Length 4;

Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 2 PTP 4

RESULT 8

US-09-009-986-31

; Sequence 31, Application US/09009986
; GENERAL INFORMATION:
; APPLICANT: REID, ROBERT H.
; APPLICANT: BOEDEKER, EDGAR C.
; APPLICANT: VAN HAMONT, JOHN
; APPLICANT: SETTERSTROM, JEAN A.
; TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC
; TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN
; TITLE OF INVENTION: BIODEGRADABLE-BIOCOMPATIBLE MICROSPHERES
; FILE REFERENCE: Army 108
; CURRENT APPLICATION NUMBER: US/09/009,986
; CURRENT FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: 08/789,734
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 08/352,944
; PRIOR FILING DATE: 1994-12-09
; PRIOR APPLICATION NUMBER: 08/034,949
; PRIOR FILING DATE: 1993-03-22
; PRIOR APPLICATION NUMBER: 07/867,301
; PRIOR FILING DATE: 1992-04-10
; PRIOR APPLICATION NUMBER: 07/805,721
; PRIOR FILING DATE: 1991-11-21
; PRIOR APPLICATION NUMBER: 07/690,485
; PRIOR FILING DATE: 1991-04-24
; PRIOR APPLICATION NUMBER: 07/521,945
; PRIOR FILING DATE: 1990-05-11
; PRIOR APPLICATION NUMBER: 07/493,597
; PRIOR FILING DATE: 1990-03-15
; PRIOR APPLICATION NUMBER: 06/590,308
; PRIOR FILING DATE: 1984-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 5

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-009-986-31

Query Match 70.0%; Score 14; DB 5; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 2 PAP 4

RESULT 9

US-09-295-996A-11

; Sequence 11, Application US/09295996A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Linderman, Russell J.
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996A-11

Query Match 70.0%; Score 14; DB 6; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 3 PAP 5

RESULT 10

US-09-295-996A-19

; Sequence 19, Application US/09295996A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Linderman, Russell J.
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996A-19

Query Match 70.0%; Score 14; DB 6; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

```
Db      3 PAP 5
RESULT 11
US-09-295-996A-27
; Sequence 27, Application US/09295996A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Linderman, Russell J.
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996A-27

Query Match      70.0%; Score 14; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      2 PXP 4
Db      3 PAP 5
RESULT 12
US-09-295-996A-33
; Sequence 33, Application US/09295996A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Linderman, Russell J.
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996A-33

Query Match      70.0%; Score 14; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      2 PXP 4
Db      3 PAP 5
RESULT 13
US-09-295-996A-46
; Sequence 46, Application US/09295996A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Linderman, Russell J.
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996A-46

Query Match      70.0%; Score 14; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      2 PXP 4
Db      3 PAP 5
RESULT 14
US-09-295-996A-50
; Sequence 50, Application US/09295996A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Linderman, Russell J.
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996A-50

Query Match      70.0%; Score 14; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      2 PXP 4
Db      3 PAP 5
RESULT 15
US-09-295-996A-51
; Sequence 51, Application US/09295996A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Linderman, Russell J.
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-295-996A-51
```

; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996A-51

Query Match 70.0%; Score 14; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. NO. 2.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PXP 4
Db 3 PAP 5

Search completed: March 15, 2002, 14:31:52
Job time: 561 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:29:47 ; Search time 352.97 Seconds
(without alignments)
6.293 Million cell updates/sec

Title: US-09-988-792-12
Perfect score: 20
Sequence: 1 XPXPXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues
Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main: *
1: /cgn2_6/ptodata/2/paa/PTCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	14	70.0	3	1	PCT-US00-08879-26
2	14	70.0	3	1	PCT-US00-08879A-26
3	14	70.0	3	16	US-09-295-846A-34
4	14	70.0	3	16	US-09-295-846B-34
5	14	70.0	3	16	US-09-295-846B-27
6	14	70.0	3	16	US-09-295-924B-27
7	14	70.0	3	16	US-09-295-924B-28
8	14	70.0	3	16	US-09-295-996-38
9	14	70.0	3	16	US-09-296-113A-31

10	14	70.0	3	16	US-09-296-113B-31	Sequence 31, Appl
11	14	70.0	3	19	US-09-551-737-34	Sequence 34, Appl
12	14	70.0	3	19	US-09-551-737B-34	Sequence 34, Appl
13	14	70.0	3	19	US-09-551-738-31	Sequence 31, Appl
14	14	70.0	3	19	US-09-551-738A-31	Sequence 31, Appl
15	14	70.0	4	1	PCT-US01-12336-175	Sequence 175, App
16	14	70.0	4	1	PCT-US01-12336-176	Sequence 176, App
17	14	70.0	4	1	PCT-US01-12336-177	Sequence 177, App
18	14	70.0	4	3	US-07-884-495-2	Sequence 2, Appl
19	14	70.0	4	7	US-08-374-888A-40	Sequence 40, Appl
20	14	70.0	4	9	US-08-566-196-7	Sequence 7, Appl
21	14	70.0	4	9	US-08-569-578-20	Sequence 20, Appl
22	14	70.0	4	10	US-08-624-190-20	Sequence 20, Appl
23	14	70.0	4	11	US-08-759-397A-18	Sequence 18, Appl
24	14	70.0	4	11	US-08-761-902D-71	Sequence 71, Appl
25	14	70.0	4	11	US-08-761-902E-71	Sequence 71, Appl
26	14	70.0	4	12	US-08-897-556A-102	Sequence 102, App
27	14	70.0	4	19	US-09-547-693-175	Sequence 175, App
28	14	70.0	4	19	US-09-547-693-176	Sequence 176, App
29	14	70.0	4	19	US-09-547-693-177	Sequence 177, App
30	14	70.0	4	22	US-09-852-910-171	Sequence 171, App
31	14	70.0	5	1	PCT-US00-08879-6	Sequence 6, Appl
32	14	70.0	5	1	PCT-US00-08879-13	Sequence 13, Appl
33	14	70.0	5	1	PCT-US00-08879-22	Sequence 22, Appl
34	14	70.0	5	1	PCT-US00-08879-45	Sequence 45, Appl
35	14	70.0	5	1	PCT-US00-08879-46	Sequence 46, Appl
36	14	70.0	5	1	PCT-US00-08879-47	Sequence 47, Appl
37	14	70.0	5	1	PCT-US00-08879A-6	Sequence 6, Appl
38	14	70.0	5	1	PCT-US00-08879A-13	Sequence 13, Appl
39	14	70.0	5	1	PCT-US00-08879A-22	Sequence 22, Appl
40	14	70.0	5	1	PCT-US00-08879A-45	Sequence 45, Appl
41	14	70.0	5	1	PCT-US00-08879A-46	Sequence 46, Appl
42	14	70.0	5	1	PCT-US00-08879A-47	Sequence 47, Appl
43	14	70.0	5	1	PCT-US93-01960-5	Sequence 5, Appl
44	14	70.0	5	3	US-07-868-352-5	Sequence 5, Appl
45	14	70.0	5	7	US-08-374-540-122	Sequence 122, App

ALIGNMENTS

RESULT 1
PCT-US00-08879-26
; Sequence 26, Application PC/TUS0008879
; GENERAL INFORMATION:
; APPLICANT: Bennett, John
; APPLICANT: Brandt, Alan
; APPLICANT: Borovski, Dov
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879-26

Query Match 70.0%; Score 14; DB 1; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PXP 4
Db 1 PAP 3

```
RESULT 2
PCT-US00-08879A-26
; Sequence 26, Application PC/TUS0008879A
; GENERAL INFORMATION:
; APPLICANT: Insect Biotechnology, Inc.
; TITLE OF INVENTION: Compositions and Methods for Controlling Pests
; FILE REFERENCE: 4137-120 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/08879A
; PRIOR APPLICATION NUMBER: 09/295,924
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF Analogue
PCT-US00-08879A-26

Query Match          70.0%; Score 14; DB 1; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PXP 4
   | |
Db 1 PAP 3

RESULT 3
US-09-295-846B-34
; Sequence 34, Application US/09295846
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223
; CURRENT APPLICATION NUMBER: US/09/295,846
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF or NPF
US-09-295-846B-34

Query Match          70.0%; Score 14; DB 1; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PXP 4
   | |
Db 1 PAP 3

RESULT 4
US-09-295-846A-34
; Sequence 34, Application US/09295846A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223
; CURRENT APPLICATION NUMBER: US/09/295,846A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF or NPF
US-09-295-846A-34

Query Match          70.0%; Score 14; DB 16; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PXP 4
   | |
Db 1 PAP 3

RESULT 5
US-09-295-846B-34
; Sequence 34, Application US/09295846B
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223
; CURRENT APPLICATION NUMBER: US/09/295,846B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF or NPF
US-09-295-846B-34

Query Match          70.0%; Score 14; DB 16; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PXP 4
   | |
Db 1 PAP 3

RESULT 6
US-09-295-924B-27
; Sequence 27, Application US/09295924B
; GENERAL INFORMATION:
; APPLICANT: John, Bennett
; APPLICANT: Alan, Brandt
; APPLICANT: Dov, Borovski
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS
; FILE REFERENCE: 4137-120
; CURRENT APPLICATION NUMBER: US/09/295,924B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: TMOF analog
US-09-295-924B-27
```



```
Query Match      70.0%; Score 14; DB 16; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
  | |
Db 1 PAP 3

RESULT 7
US-09-924B-28
; Sequence 28, Application US/09295924B
; GENERAL INFORMATION:
; APPLICANT: John, Bennett
; APPLICANT: Alan, Brandt
; APPLICANT: Dov, Borovski
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS
; FILE REFERENCE: 4137-120
; CURRENT APPLICATION NUMBER: US/09/295,924B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature
; LOCATION: ().()
; OTHER INFORMATION: TMOF analog
US-09-295-924B-28

Query Match      70.0%; Score 14; DB 16; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
  | |
Db 1 PAP 3

RESULT 8
US-09-295-996-38
; Sequence 38, Application US/09295996
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: NOVEL PEPTIDES AND THE USE THEREOF TO CONTROL PESTS
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: unknown
US-09-295-996-38

Query Match      70.0%; Score 14; DB 16; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
  | |
Db 1 PAP 3

RESULT 9
US-09-296-113A-31
; Sequence 31, Application US/09296113A
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect
; TITLE OF INVENTION: Larvae
; FILE REFERENCE: UF-224
; CURRENT APPLICATION NUMBER: US/09/296,113A
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF or NPF
; OTHER INFORMATION: fragment
US-09-296-113A-31

Query Match      70.0%; Score 14; DB 16; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
  | |
Db 1 PAP 3

RESULT 10
US-09-296-113B-31
; Sequence 31, Application US/09296113B
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect
; TITLE OF INVENTION: Larvae
; FILE REFERENCE: UF-224
; CURRENT APPLICATION NUMBER: US/09/296,113B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF or NPF
; OTHER INFORMATION: fragment
US-09-296-113B-31

Query Match      70.0%; Score 14; DB 16; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
  | |
Db 1 PAP 3

RESULT 11
US-09-551-737-34
; Sequence 34, Application US/09551737
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Schlesinger, Yaaqov
; APPLICANT: Nauwelaers, Sabine M.I.
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223C1
; CURRENT APPLICATION NUMBER: US/09/551,737
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/295,846
; PRIOR FILING DATE: 1999-04-21
```

; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 34
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: TMOF or NPf
 ; OTHER INFORMATION: fragment
 US-09-551-737-34

Query Match 70.0%; Score 14; DB 19; Length 3;
 Best Local Similarity 66.7%; Pred. No. 2.9e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 1 PAP 3

RESULT 12
 US-09-551-737B-34
 ; Sequence 34, Application US/09551737B
 ; GENERAL INFORMATION:
 ; APPLICANT: Borovsky, Dov
 ; APPLICANT: Nauwelaers, Sabine M. I.
 ; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
 ; FILE REFERENCE: UF-224C1
 ; CURRENT APPLICATION NUMBER: US/09/551.737B
 ; CURRENT FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: US 09/295,846
 ; PRIOR FILING DATE: 1999-04-21
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 34
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: TMOF peptide
 US-09-551-737B-34

Query Match 70.0%; Score 14; DB 19; Length 3;
 Best Local Similarity 66.7%; Pred. No. 2.9e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 1 PAP 3

RESULT 13
 US-09-551-738-31
 ; Sequence 31, Application US/09551738
 ; GENERAL INFORMATION:
 ; APPLICANT: Borovsky, Dov
 ; TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect
 ; FILE REFERENCE: UF-224C1
 ; CURRENT APPLICATION NUMBER: US/09/551.738
 ; CURRENT FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: 09/296,113
 ; PRIOR FILING DATE: 1999-04-21
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: TMOF or NPf
 ; OTHER INFORMATION: fragment
 US-09-551-738-31

Query Match 70.0%; Score 14; DB 19; Length 3;
 Best Local Similarity 66.7%; Pred. No. 2.9e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 1 PAP 3

RESULT 14
 US-09-551-738A-31
 ; Sequence 31, Application US/09551738A
 ; GENERAL INFORMATION:
 ; APPLICANT: Borovsky, Dov
 ; TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
 ; FILE REFERENCE: UF-224C1
 ; CURRENT APPLICATION NUMBER: US/09/551.738A
 ; CURRENT FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: US 09/296,113
 ; PRIOR FILING DATE: 1999-04-21
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: TMOF peptide
 US-09-551-738A-31

Query Match 70.0%; Score 14; DB 19; Length 3;
 Best Local Similarity 66.7%; Pred. No. 2.9e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 1 PAP 3

RESULT 15
 PCT-US01-12336-175
 ; Sequence 175, Application PC/TUS0112336
 ; GENERAL INFORMATION:
 ; APPLICANT: Kieliszewski, Marcia
 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
 ; FILE REFERENCE: GHU-06319
 ; CURRENT APPLICATION NUMBER: PCT/US01/12336
 ; CURRENT FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 09/547,693
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 244
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 175
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; NAME/KEY: SITE
 ; LOCATION: (2)..(2)
 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
 ; NAME/KEY: SITE
 ; LOCATION: (4)..(4)
 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
 PCT-US01-12336-175

Query Match 70.0%; Score 14; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 2 PSP 4

Search completed: March 15, 2002, 14:29:47
Job time: 531 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:22:28 ; Search time 66.25 Seconds
(without alignments)
12.299 Million cell updates/sec

Title: US-09-988-792-13
Perfect score: 57
Sequence: 1 RPKPQQPFGLX 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	56	98.2	10	22	AAB91423	Tachykinins peptid
2	56	98.2	10	22	AAB91427	Tachykinins peptid
3	56	98.2	11	7	AAP61480	Sequence of undeca
4	56	98.2	11	9	AAP80312	Sequence of neurope
5	56	98.2	11	12	AAR13162	Sialic acid-bonded
6	56	98.2	11	12	AAR11854	Undeceptide subs
7	56	98.2	11	13	AAR21936	Substance p or (7-
8	56	98.2	11	13	AAR21937	Substance p or (7-
9	56	98.2	11	13	AAR21938	Substance p [Me-Ie
10	56	98.2	11	13	AAR21942	Substance p [MeMet
11	56	98.2	11	13	AAR21944	Substance p [Pro 1

12	56	98.2	11	13	AAR21946	Substance p [Me-Ph
13	56	98.2	11	13	AAR21954	Substance p [Me-Gl
14	56	98.2	11	13	AAR21962	Substance p [Me-Gl
15	56	98.2	11	13	AAR21963	Substance p [p-Chl
16	56	98.2	11	13	AAR28442	Substance p, Synt
17	56	98.2	11	14	AAR42646	Neurokinin 1 recep
18	56	98.2	11	16	AAR85243	Substance p peptid
19	56	98.2	11	16	AAW09003	Substance p analog
20	56	98.2	11	16	AAR77310	Substance p, Synt
21	56	98.2	11	18	AAW33180	Mono-DTPA-Argi Sub
22	56	98.2	11	18	AAW04616	Substance p peptid
23	56	98.2	11	19	AAW42973	Substrate p report
24	56	98.2	11	20	AAW30985	Non-crosslinked pr
25	56	98.2	11	20	AAW03156	Substance p, Synt
26	56	98.2	11	20	AAW99689	Substance p analog
27	56	98.2	11	20	AAW92709	Human tachykinin a
28	56	98.2	11	20	AAW92715	Human tachykinin a
29	56	98.2	11	20	AAW92717	Human tachykinin a
30	56	98.2	11	20	AAW92718	Human tachykinin a
31	56	98.2	11	20	AAW92719	Human tachykinin a
32	56	98.2	11	20	AAW92720	Human tachykinin a
33	56	98.2	11	20	AAW92708	Human tachykinin a
34	56	98.2	11	20	AAW92680	Human tachykinin a
35	56	98.2	11	20	AAW92681	Human tachykinin a
36	56	98.2	11	20	AAW92667	Human tachykinin a
37	56	98.2	11	20	AAW92668	Human tachykinin a
38	56	98.2	11	20	AAW92676	Human tachykinin a
39	56	98.2	11	20	AAW92731	Human tachykinin a
40	56	98.2	11	20	AAW79662	Substance p deriva
41	56	98.2	11	20	AAW79663	Substance p deriva
42	56	98.2	11	21	AAH18483	Peptide substrate
43	56	98.2	11	21	AAH23027	Human/rat tachykin
44	56	98.2	11	21	AAH23382	Cell differentiat
45	56	98.2	11	22	AAH98866	Chimeric analgesic

ALIGNMENTS

RESULT 1
AAB91423 standard; Peptide; 10 AA.
ID AAB91423 standard; Peptide; 10 AA.
XX
AC AAB91423;
XX
XX
DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:599.
DE
DE Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotrausmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA Sialic acid-bonded
XX Undeceptide subs
XX Substance p or (7-
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

PT Disclosure; Page 395; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.

XX Sequence 10 AA;

SQ

Query Match 98.2%; Score 56; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGL 10
 |||||

Db 1 rpkpqffgl 10

RESULT 2

AAB91427

ID AAB91427 standard; Peptide; 10 AA.

XX

AC AAB91427;

XX

DT 22-JUN-2001 (first entry)

XX

DE Tachykinins peptide SEQ ID NO:603.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 blood component; modification; succinimidyl; maleimido group; amino;
 hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO2000069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US13576.

XX

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX

PA (CONJ-) CONJUCHEM INC.

XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX

DR WPI; 2001-112059/12.

XX

PT Modifying and attaching therapeutic peptides to albumin prevents
 peptidase degradation, useful for increasing length of in vivo activity

PT Disclosure; Page 396; 733pp; English.

PS

XX

CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.

XX Sequence 10 AA;

SQ

Query Match 98.2%; Score 56; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQOFFGL 10
 |||||

Db 1 rpkpqffgl 10

RESULT 3

AAP61480

ID AAP61480 standard; peptide; 11 AA.

XX

AC AAP61480;

XX

DT 22-AUG-1991 (first entry)

XX

DE Sequence of undeca peptide substance P1.

XX

KW Hypertension therapy; sleep disorder; anti-stress agent.

XX

FH Key Location/Qualifiers

FT Misc-difference 11

FT /label= Met-NH2

PN DD229593-A.

XX

PD 13-NOV-1985.

XX

PF 28-NOV-1984; 84DD-0269954.

XX

PR 28-NOV-1984; 84DD-0269954.

XX

PA (DEAK) AKAD WISSENSCHAFT DDR.

XX

PI Oehme P, Hecht K, Wachtel E, Roske I, Kolometsewa IA;
 Airapetjan M, Bienert M, Vogt WE, Hilse H, Gores E, Poppei M;
 Nieber K, Bergmann J;

XX

DR WPI; 1986-069587/11.

XX

XX Cpd. having N-terminal sequences of undeca:peptide substance P -
 are medicinal agents with anti-stress activity

PT

PS Claim 1; Page 1; 15pp; German.

XX

CC The inventors claim an antistress compound which contains the N-terminal SQ of AAP61480, pref. Arg-Pro-Lys-Pro-X (X= COOH or NH2). Compared with the full undecapeptide they have much reduced side effects (acute hypotension, spastic effects on the ileum and histamine release from peritoneal mast cells).

CC

XX
SQ Sequence 11 AA;

Query Match 98.2%; Score 56; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
| | | | | | | | | |
Db 1 rpkpqffgl 10

RESULT 4
AAP80312
ID AAP80312 standard; protein; 11 AA.

XX
AC AAP80312;

XX
DT 14-SEP-1990 (first entry)

XX
DE Sequence of neuro peptide substance P which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX
KW Spantide; neuro peptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW substance P.

XX
OS Swiss 3T3 cells.

XX
FH Key Location/Qualifiers
FT Misc-difference 11
FT /label=OTHER
FT /note="Met-NH2"

XX
PN W08807551-A.

XX
PD 06-OCT-1988.

XX
PF 31-MAR-1988; 88WO-GB00255.

XX
PR 25-NOV-1987; 87GB-0027638.

XX
PA (IMCR) IMPERIAL CANCER RES.

XX
PI Rosengurt E, Zachary I, Woll P;

XX
PS WPI; 1988-292842/41.

XX
PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation

XX
PS Disclosure; Table 2; 42pp; English.

XX
CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist B. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Arg1, D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.

XX
SQ Sequence 11 AA;

Query Match 98.2%; Score 56; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
| | | | | | | | | |
Db 1 rpkpqffgl 10

RESULT 5
AAR13162
ID AAR13162 standard; Protein; 11 AA.

XX
AC AAR13162;

XX
DT 10-OCT-1991 (first entry)

XX
DE Sialic acid-bonded polypeptide (2).

XX
KW Sialic acid; cataract; immune disorder.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminally glycosylated by 5-acetamido-

FT 2,4,7,8,9-penta-O-acetyl-3,5-deoxy-beta-
FT D-glycero-D-galactononulopyranosyl"

XX
PN JP03151398-A.

XX
PD 27-JUN-1991.

XX
PF 06-NOV-1989; 89JP-0288560.

XX
PR 06-NOV-1989; 89JP-0288560.

XX
PA (MECT-) MECT KK.

XX
DR WPI; 1991-233839/32.

XX
PT New sialic acid derivs. bonded to physiologically active
PT polypeptide - for treatment of cataracts, immune disorders etc.
PT with prolonged half-life

XX
PS Example 4; Page 6; 7pp; Japanese.

XX
CC The prod. has prolonged half-life and is used as a pharmaceutical
CC for treatment of various diseases, such as cataract and immune
CC disorders. It comprises a peptide, N-terminally glycosylated by
CC (opt. acetylated) sialic acid.

XX
CC See also AAR12932, AAR13162 and AAR13201.

XX
SQ Sequence 11 AA;

Query Match 98.2%; Score 56; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
| | | | | | | | | |
Db 1 rpkpqffgl 10

RESULT 6

AAR11854

ID AAR11854 standard; peptide; 11 AA.

XX
AC AAR11854;

XX

DT 09-JUL-1991 (first entry)
 XX Undecapeptide substance P.
 DE Undecapeptide; pharmaceutical; stress; sleep.
 XX Synthetic.
 KW DD285097-A.
 XX 05-DEC-1990.
 PD 21-JUN-1989; 89DD-0329831.
 PF 21-JUN-1989; 89DD-0329831.
 XX 21-JUN-1989; 89DD-0329831.
 XX (DEAK) INST WIRKSTOFF AKAD.
 PA (FARF) VEB CHEM BITTERFELD.
 XX Beyermann M, Bienert M, Egler H, Haupke K, Krause E;
 PI Schwarz J, Walz H;
 PI WPI; 1991-133498/19.
 DR Undeca-peptide substance pharmaceutical intermediate prepn. - by
 PT forming di:peptide between nitro-arginine and proline and
 PT reacting with polymer-bound non-peptide
 XX Calim 1; Page 1; 8pp; German.
 XX The peptide is prepared by solid phase synthesis.
 CC It can be used in the preparation of pharmaceuticals which can be
 CC used to treat certain stress-induced disturbances of the sleep
 CC profile.
 XX Sequence 11 AA;
 SQ

Query Match 98.2%; Score 56; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RPKPQQFFGL 10
 DB 1 rpkpqffgl 10

RESULT 7
 AAR21936
 ID AAR21936 standard; Protein; 11 AA.
 XX AAR21936;
 AC 25-JUN-1992 (first entry)
 DT Substance P or (7-11) [Ethionine 11].
 DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 XX syndrome; hereditary cerebral haemorrhage.
 KW Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 11
 FT /label= OTHER
 FT /note= "OTHER = Ethionine"
 XX WO9202248-A.
 PN 20-FEB-1992.
 XX 29-JUL-1991; 91WO-US05323.
 XX Treatment of neuronal accumulation of beta-amyloid - using

PR 27-JUL-1990; 90US-0559173.
 XX (CHIL-) CHILDRENS MED CENT.
 PA Yankner BA;
 PI WPI; 1992-079804/10.
 XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX Claim 10; Page 21; 35pp; English.
 XX The peptide is the tachykinin agonist substance P with an Ethionine
 CC residue substituted at position 11. The peptide was synthesised
 CC by standard solid phase synthesis. An N-terminal deleted peptide
 CC (7-11) with the same substitution was also synthesised. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptides can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 XX Sequence 11 AA;
 SQ

Query Match 98.2%; Score 56; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RPKPQQFFGL 10
 DB 1 rpkpqffgl 10

RESULT 8
 AAR21937
 ID AAR21937 standard; Protein; 11 AA.
 XX AAR21937;
 AC 25-JUN-1992 (first entry)
 DT Substance P or (7-11) [Norleucine 11].
 DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 XX syndrome; hereditary cerebral haemorrhage.
 KW Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 11
 FT /label= OTHER
 FT /note= "OTHER = Nle"
 XX WO9202248-A.
 PN 20-FEB-1992.
 XX 29-JUL-1991; 91WO-US05323.
 XX 27-JUL-1990; 90US-0559173.
 XX (CHIL-) CHILDRENS MED CENT.
 PA Yankner BA;
 PI WPI; 1992-079804/10.
 XX Treatment of neuronal accumulation of beta-amyloid - using

PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
PS Claim 10; Page 21; 35pp; English.
XX The peptide is the tachykinin agonist substance P with a Norleucine
CC residue substituted at position 11. The peptide was synthesised
CC by standard solid phase synthesis. An N-terminal deleted peptide
CC (7-11) with the same substitution was also synthesised. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptides can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

Query Match 98.2%; Score 56; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
Db 1 rpkpqgffgl 10
|||||

RESULT 9
AAR21938
ID AAR21938 standard; Protein; 11 AA.
XX
AC AAR21938;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Me-Leu 10].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 10
FT /label= OTHER
FT /note= "Me-Leu"

W09202248-A.
XX
PN 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 10; Page 21; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with Me-Leu
CC substituted at position 10. The peptide was synthesised
CC by standard solid phase synthesis. Neuronal accumulation of
CC beta-amyloid may be treated by administration of tachykinin

CC agonists. The peptides can reduce the neurotoxic effects of a
CC beta-amyloid related polypeptide on cultured neurons. The peptide
CC and its analogues are useful for controlling diseases characterised
CC by beta amyloid accumulation in the brain such as Alzheimer's
CC disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

Query Match 98.2%; Score 56; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
Db 1 rpkpqgffgl 10
|||||

RESULT 10
AAR21942
ID AAR21942 standard; Protein; 11 AA.
XX
AC AAR21942;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [MeMet 11].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 11
FT /label= OTHER
FT /note= "OTHER = Methyl Methionine"

W09202248-A.
XX
PN 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 10; Page 21; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a methyl
CC methionine residue substituted at position 11. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

Query Match 98.2%; Score 56; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
 |||||
 Db 1 rpkpqffgl 10

RESULT 11

AAR21944
 ID AAR21944 standard; Protein; 11 AA.
 XX AC AAR21944;

XX 25-JUN-1992 (first entry)

DE Substance P [Pro 11].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a Proline
 CC residue substituted at position 11. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match 98.2%; Score 56; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
 |||||
 Db 1 rpkpqffgl 10

RESULT 12

AAR21946
 ID AAR21946 standard; Protein; 11 AA.
 XX AC AAR21946;

XX 25-JUN-1992 (first entry)

DE Substance P [Me-Gly 9].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers

DT 25-JUN-1992 (first entry)
 XX Substance P [Me-Phe 8].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 8
 FT /label= OTHER
 FT /note= "OTHER = Methyl phenylalanine"

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI; 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a methyl
 CC phenylalanine residue substituted at position 8. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match 98.2%; Score 56; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
 |||||
 Db 1 rpkpqffgl 10

RESULT 13

AAR21954
 ID AAR21954 standard; Protein; 11 AA.
 XX AC AAR21954;

XX 25-JUN-1992 (first entry)

DE Substance P [Me-Gly 9].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 9
 FT /label= OTHER
 FT /note= "OTHER = Methyl glycine"
 PN
 XX WO9202248-A.
 XX
 PD 20-FEB-1992.
 XX
 XX 29-JUL-1991; 91WO-US05323.
 XX
 PR 27-JUL-1990; 90US-0559173.
 XX
 XX (CHIL-) CHILDRENS MED CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI; 1992-079804/10.
 DR
 XX Treatment of neuronal accumulation of beta-amyloid - using
 XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 PT
 XX Claim 10; Page 22; 35pp; English.
 PS
 XX The peptide is the tachykinin agonist substance P with a methyl
 CC glycine residue substituted at position 9. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 XX
 XX Sequence 11 AA;

Query Match 98.2%; Score 56; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 ID |||||
 Db 1 rpkpqffgl 10

RESULT 14

AAR21962
 ID AAR21962 standard; Peptide; 11 AA.

XX
 XX AC AAR21962;

XX 25-JUN-1992 (first entry)

XX Substance P [Me Gly 6, Met (O2) 11].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers

PH Misc-difference 6

FT /label= OTHER
 FT /note= "OTHER = Methyl glycine"

FT Misc-difference 11

FT /label= OTHER
 FT /note= "OTHER = Met (O2)"

XX WO9202248-A.

XX 20-FEB-1992.

PD

XX 29-JUL-1991; 91WO-US05323.
 XX
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX (CHIL-) CHILDRENS MED CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI; 1992-079804/10.
 DR
 XX Treatment of neuronal accumulation of beta-amyloid - using
 XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 PT
 XX Claim 10; Page 22; 35pp; English.
 PS
 XX The peptide is the tachykinin agonist, substance P with methyl
 CC glycine substituted at position 9 and Met (O2) at position 11.
 CC The peptide was synthesised by standard solid phase synthesis.
 CC Neuronal accumulation of beta-amyloid may be treated by administ-
 CC ration of tachykinin agonists. The peptide can reduce the neuro-
 CC toxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 XX
 XX Sequence 11 AA;

Query Match 98.2%; Score 56; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 ID |||||
 Db 1 rpkpqffgl 10

RESULT 15

AAR21963
 ID AAR21963 standard; Peptide; 11 AA.

XX
 XX AC AAR21963;

XX 25-JUN-1992 (first entry)

XX Substance P [p-Chloro-Phe 7,8].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers

PH Modified-site 7

FT /label= OTHER
 FT /note= "OTHER = p-Chloro-phenylalanine"

FT Modified-site 8

FT /label= OTHER
 FT /note= "OTHER = p-Chloro-phenylalanine"

XX WO9202248-A.

XX 20-FEB-1992.

PD

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX

PI Yankner BA;
 XX
 DR WPI; 1992-079804/10.
 XX
 XX
 PT Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 XX
 PS Claim 10; Page 22; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist, substance P fragment
 CC with p-chloro-phenylalanine residues substituted at positions 7 and
 CC 8. The peptide was synthesised by standard solid phase synthesis.
 CC Neuronal accumulation of beta-amyloid may be treated by administ-
 CC ration of tachykinin agonists. The peptide can reduce the neuro-
 CC toxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 XX
 SQ Sequence 11 AA;

Query Match 98.2%; Score 56; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGL 10
 Db 1 RPKPQOFFGL 10

Search completed: March 15, 2002, 14:22:28
 Job time: 368 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:23:06 ; Search time 32.16 seconds
(without alignments)
5.598 Million cell updates/sec

Title: US-09-988-792-12
Perfect score: 20
Sequence: 1 XPXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	70.0	4	1	US-07-917-034A-3
2	14	70.0	4	1	US-07-917-034A-4
3	14	70.0	4	1	US-07-917-034A-5
4	14	70.0	4	2	US-08-666-473-30
5	14	70.0	4	2	US-08-747-137-136
6	14	70.0	4	2	US-08-978-096-7
7	14	70.0	4	3	US-09-195-868-18
8	14	70.0	4	4	US-09-303-965-7
9	14	70.0	4	4	US-08-895-590-40
10	14	70.0	5	1	US-07-708-035-5
11	14	70.0	5	1	US-07-708-035-6
12	14	70.0	5	1	US-07-708-035-8
13	14	70.0	5	1	US-07-708-035-9
14	14	70.0	5	1	US-07-708-035-10
15	14	70.0	5	1	US-07-708-035-11
16	14	70.0	5	1	US-07-708-035-15
17	14	70.0	5	1	US-07-989-290-1
18	14	70.0	5	1	US-07-917-034A-2
19	14	70.0	5	1	US-07-917-034A-7
20	14	70.0	5	1	US-08-271-698-1
21	14	70.0	5	1	US-08-328-536-5
22	14	70.0	5	1	US-08-468-596-1
23	14	70.0	5	1	US-08-704-170-91
24	14	70.0	5	2	US-08-666-473-31
25	14	70.0	5	2	US-08-437-013-22
26	14	70.0	5	2	US-08-437-013-23
27	14	70.0	5	2	US-08-437-013-25

28	14	70.0	5	4	US-08-810-712-12	Sequence 12, Appl
29	14	70.0	5	4	US-08-134-198E-38	Sequence 38, Appl
30	14	70.0	5	5	PCT-US94-02631-91	Sequence 91, Appl
31	14	70.0	6	1	US-07-989-290-2	Sequence 2, Appl
32	14	70.0	6	1	US-07-917-034A-8	Sequence 8, Appl
33	14	70.0	6	1	US-07-917-034A-14	Sequence 14, Appl
34	14	70.0	6	1	US-08-072-063-5	Sequence 5, Appl
35	14	70.0	6	1	US-08-271-698-2	Sequence 2, Appl
36	14	70.0	6	1	US-08-205-938A-5	Sequence 5, Appl
37	14	70.0	6	1	US-08-205-938A-6	Sequence 6, Appl
38	14	70.0	6	1	US-08-468-596-2	Sequence 2, Appl
39	14	70.0	6	1	US-08-064-693-5	Sequence 5, Appl
40	14	70.0	6	1	US-08-596-116A-40	Sequence 40, Appl
41	14	70.0	6	1	US-08-596-116A-41	Sequence 41, Appl
42	14	70.0	6	1	US-08-596-116A-42	Sequence 42, Appl
43	14	70.0	6	2	US-08-609-046A-3	Sequence 3, Appl
44	14	70.0	6	2	US-08-666-473-32	Sequence 32, Appl
45	14	70.0	6	2	US-08-850-910A-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-07-917-034A-3
; Sequence 3, Application US/07917034A
; Patent No. 5427927
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas, Pohliner, Johannes, Schumacher,
; APPLICANT: G nter, Dony, Carola
; TITLE OF INVENTION: Process For The Enzymatic Cleavage
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; Zip: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/917,034A
FILING DATE: 19920830
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00192
FILING DATE: 1-Feb-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 39 415.8
FILING DATE: 10-Dec-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 922.1
FILING DATE: 17-May-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 921.3
FILING DATE: 17-May-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 03 149.7
FILING DATE: 3-Feb-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5427927man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: HUBR 1018
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-917-034A-3

Query Match 70.0%; Score 14; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 2 PXP 4
| |
Db 2 PSP 4

RESULT 2

US-07-917-034A-4
; Sequence 4, Application US/07917034A
; Patent No. 5427927
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas, Pohlner, Johannes, Schumacher,
; APPLICANT: G nter, Dony, Carola
; TITLE OF INVENTION: Process For The Enzymatic Cleavage
; TITLE OF INVENTION: of Recombinant Proteins Using Iga Proteases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/917.034A
FILING DATE: 19920830
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00192
FILING DATE: 1-Feb-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 39 415.8
FILING DATE: 10-Dec-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 922.1
FILING DATE: 17-May-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 921.3
FILING DATE: 17-May-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 03 149.7
FILING DATE: 3-Feb-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5427927man D.
REGISTRATION NUMBER: 30,946

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-917-034A-4

Query Match 70.0%; Score 14; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 2 PXP 4
| |

Db 2 PAP 4

RESULT 3

US-07-917-034A-5
; Sequence 5, Application US/07917034A
; Patent No. 5427927
; GENERAL INFORMATION:
; APPLICANT: Meyer, Thomas, Pohlner, Johannes, Schumacher,
; APPLICANT: G nter, Dony, Carola
; TITLE OF INVENTION: Process For The Enzymatic Cleavage
; TITLE OF INVENTION: of Recombinant Proteins Using Iga Proteases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/917.034A
FILING DATE: 19920830
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00192
FILING DATE: 1-Feb-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 39 415.8
FILING DATE: 10-Dec-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 922.1
FILING DATE: 17-May-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 921.3
FILING DATE: 17-May-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 03 149.7
FILING DATE: 3-Feb-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5427927man D.
REGISTRATION NUMBER: 30,946

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-917-034A-5

Query Match 70.0%; Score 14; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 2 PXP 4
| |
Db 2 PTP 4

RESULT 4

US-08-666-473-30
; Sequence 30, Application US/08666473
; Patent No. 5843713
; GENERAL INFORMATION:
; APPLICANT: YOSHIDA, Aruto
; APPLICANT: TAKEUCHI, Makoto

;; TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
;; TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
;; TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
;; NUMBER OF SEQUENCES: 114
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/666,473
;; FILING DATE: 19-SEP-1996
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/JP95/02238
;; FILING DATE: 01-NOV-1995
;;
;; APPLICATION DATA:
;; APPLICATION NUMBER: JP 7-22101
;; FILING DATE: 09-FEB-1995
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 6-269111
;; FILING DATE: 01-NOV-1994
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 16887/837
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;;
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-08-666-473-30

Query Match 70.0%; Score 14; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 2 PXP 4
Db 2 PAP 4

RESULT 5
US-08-747-137-136
; Sequence 136, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/747,137
;; FILING DATE: 12-NOV-1996
;; CLASSIFICATION: 424
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/212,546
;; FILING DATE: 14-MAR-1994
;;
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 08/069,831
;; FILING DATE: 01-JUN-1993
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/959,560
;; FILING DATE: 13-OCT-1992
;;
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/641,720
;; FILING DATE: 15-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 016197-000840US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-576-0200
;; INFORMATION FOR SEQ ID NO: 136:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 4
;; OTHER INFORMATION: /product= "Ser-Amide"
;;
;; US-08-747-137-136

Query Match 70.0%; Score 14; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 2 PXP 4
Db 1 PTP 3

RESULT 6
US-08-978-096-7
; Sequence 7, Application US/08978096
; Patent No. 5948886
; GENERAL INFORMATION:
; APPLICANT: Peet, No. 5948886ton P.
; APPLICANT: Burkhardt, Joseph P.
; APPLICANT: Mehdi, Shujaath
; TITLE OF INVENTION: Acylated Enol Derivatives of
; TITLE OF INVENTION: alpha-ketoesters and alpha-ketoamides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoechst Marion Roussel, Inc.
; STREET: 2110 E. Galbraith Road, P.O. Box 156300
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,096
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA: 08/566,196
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Boudreaux, William R.
REGISTRATION NUMBER: 35,796
REFERENCE/DOCKET NUMBER: M01838
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513/948-6566
TELEFAX: 513/948-7961 or 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-978-096-7

Query Match 70.0%; Score 14; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 1 PAP 3

RESULT 7
US-09-195-868-18
; Sequence 18, Application US/09195868
; Patent No. 6090621
; GENERAL INFORMATION:
; APPLICANT: KAVANAUGH MD, MICHAEL
; APPLICANT: POT PH.D., DAVID
; APPLICANT: WILLIAMS MDPHD, LEWIS T.
; TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
; TITLE OF INVENTION: 5-PHOSPHATASES (SIPs)
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FIRESTONE, LEIGH H.
; REGISTRATION NUMBER: 36,831
; REFERENCE/DOCKET NUMBER: 1182.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-923-2707
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-195-868-18

Query Match 70.0%; Score 14; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 2 PTP 4

RESULT 8
US-09-303-965-7
; Sequence 7, Application US/09303965
; Patent No. 6172044
; GENERAL INFORMATION:
; APPLICANT: Peet, No. 6172044ton P.
; APPLICANT: Burkhardt, Joseph P.
; APPLICANT: Mehdi, Shujaath
; TITLE OF INVENTION: Aclated Enol Derivatives of
; TITLE OF INVENTION: alpha-ketoesters and alpha-Ketoamides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoechst Marion Roussel, Inc.
; STREET: 2110 E. Galbraith Road, P.O. Box 156300
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,965
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/566,196
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Boudreaux, William R.
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01838
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513/948-6566
; TELEFAX: 513/948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-965-7

Query Match 70.0%; Score 14; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 1 PAP 3

RESULT 9
US-08-895-590-40
; Sequence 40, Application US/08895590
; Patent No. 6207410
; GENERAL INFORMATION:

APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/895,590
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/374,888
APPLICATION NUMBER: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 022650-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-895-590-40

Query Match 70.0%; Score 14; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 1 PTP 3

RESULT 10
US-07-708-035-5
; Sequence 5, Application US/07708035
; Patent No. 5215964
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; APPLICANT: Audhya, Tapan
; APPLICANT: Heavner, George
; APPLICANT: Anwer, Mohmad K.
; TITLE OF INVENTION: Peptides Useful in Regulating The Immune
; TITLE OF INVENTION: and Nervous Systems
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: 321 No. 5215964ristown Road, Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,035
FILING DATE: 19910603
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IRIP-US40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Acetyl
OTHER INFORMATION: /note= "Acetyl is attached to amino terminus of
OTHER INFORMATION: peptide."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= NH2
OTHER INFORMATION: /note= "NH2 is attached to carboxy terminus of
OTHER INFORMATION: peptide."
US-07-708-035-5

Query Match 70.0%; Score 14; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 2 PAP 4

RESULT 11
US-07-708-035-6
; Sequence 6, Application US/07708035
; Patent No. 5215964
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; APPLICANT: Audhya, Tapan
; APPLICANT: Heavner, George
; APPLICANT: Anwer, Mohmad K.
; TITLE OF INVENTION: Peptides Useful in Regulating The Immune
; TITLE OF INVENTION: and Nervous Systems
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: 321 No. 5215964ristown Road, Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/708,035
; FILING DATE: 19910603
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.

```
Query Match          70.0%; Score 14; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy	2	PXP	4
Db	2	PSP	4

```

13
US-07-708-035-9
; Sequence 9, Application US/07708035
; Patent No. 5215964
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; APPLICANT: Audhya, Tapan
; APPLICANT: Heavner, George
; APPLICANT: Anwer, Mohammad K.
; TITLE OF INVENTION: Peptides Useful in Regulating The Immune
; TITLE OF INVENTION: and Nervous Systems
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: 321 No. 5215964ristown Road, Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07708,035
; FILING DATE: 19910603
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: IRIP-US40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; TELEX: 910-250-6892
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site

```

; LOCATION: 1
; OTHER INFORMATION: /label= Acetyl
; /note= "Acetyl is attached to amino terminus of
; peptide."
; OTHER INFORMATION: peptide."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= NH2
; /note= "NH2 is attached to amino terminus of
; peptide."
; OTHER INFORMATION: peptide."
US-07-708-035-9

Query Match 70.0%; Score 14; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. NO. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 2 PTP 4

RESULT 14
US-07-708-035-10
; Sequence 10, Application US/07708035
; Patent No. 5215964
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; APPLICANT: Audhya, Tapan
; APPLICANT: Heavner, George
; APPLICANT: Anwer, Mohmad K.
; TITLE OF INVENTION: Peptides Useful in Regulating The Immune
; and Nervous Systems
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: 321 No. 5215964ristown Road, Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/708,035
; FILING DATE: 19910603
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: IRIP-US40
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; TELEX: 910-250-6892
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetyl
; /note= "Acetyl is attached to the amino terminus
; of the peptide."
; OTHER INFORMATION: of the peptide."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5

; OTHER INFORMATION: /label= NH2
; OTHER INFORMATION: /note= "NH2 is attached to the carboxy terminus of
; the peptide."
; OTHER INFORMATION: the peptide."
US-07-708-035-10

Query Match 70.0%; Score 14; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. NO. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
| |
Db 2 PTP 4

RESULT 15
US-07-708-035-11
; Sequence 11, Application US/07708035
; Patent No. 5215964
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; APPLICANT: Audhya, Tapan
; APPLICANT: Heavner, George
; APPLICANT: Anwer, Mohmad K.
; TITLE OF INVENTION: Peptides Useful in Regulating The Immune
; and Nervous Systems
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: 321 No. 5215964ristown Road, Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/708,035
; FILING DATE: 19910603
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: IRIP-US40
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; TELEX: 910-250-6892
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetyl
; /note= "Acetyl is attached to amino terminus of
; the peptide."
; OTHER INFORMATION: peptide."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= NH2
; /note= "NH2 is attached to the carboxy terminus of
; the peptide."
; OTHER INFORMATION: the peptide."
US-07-708-035-11

Query Match 70.0%; Score 14; DB 1; Length 5;

Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
1 1
Db 2 PSP 4

Search completed: March 15, 2002, 14:23:06
Job time: 216 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:22:27 ; Search time 66.25 Seconds
(without alignments)
8.945 Million cell updates/sec

Title: US-09-988-792-12
Perfect score: 20
Sequence: 1 XPXPXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	ID	Description
1	14	70.0	3	21 AAB37933	Trypsin modulating
2	14	70.0	4	14 AAR38441	Diuretic hormone b
3	14	70.0	4	14 AAR38442	Diuretic hormone b
4	14	70.0	4	14 AAR38447	Diuretic hormone b
5	14	70.0	4	14 AAR38448	Diuretic hormone b
6	14	70.0	4	19 AAW58698	Antigen epitope re
7	14	70.0	4	20 AAY33350	Elastase inhibitor
8	14	70.0	4	20 AAY31087	Non-crosslinked pr
9	14	70.0	4	22 AAB74035	Partial sequence c
10	14	70.0	4	22 AAB46762	L-prolinamide deri
11	14	70.0	5	13 AAR29185	Immunomodulatory T

12	14	70.0	5	13 AAR29186	Immunomodulatory T
13	14	70.0	5	13 AAR29188	Immunomodulatory T
14	14	70.0	5	13 AAR29189	Immunomodulatory T
15	14	70.0	5	13 AAR29190	Immunomodulatory T
16	14	70.0	5	13 AAR29191	Immunomodulatory T
17	14	70.0	5	14 AAR38450	Diuretic hormone b
18	14	70.0	5	14 AAR38451	Diuretic hormone b
19	14	70.0	5	14 AAR38452	Diuretic hormone b
20	14	70.0	5	14 AAR38455	Diuretic hormone b
21	14	70.0	5	14 AAR38456	Diuretic hormone b
22	14	70.0	5	14 AAR38457	Diuretic hormone b
23	14	70.0	5	14 AAR42441	DF3 peptide antige
24	14	70.0	5	15 AAR63464	Trypsin Modulating
25	14	70.0	5	15 AAR56872	Oostatic factor in
26	14	70.0	5	15 AAR62183	U1 snRNP 70K prote
27	14	70.0	5	16 AAR80072	p1 analogue of try
28	14	70.0	5	16 AAR75517	p. communis (pear)
29	14	70.0	5	16 AAR76134	hML(2-6). Homo sa
30	14	70.0	5	17 AAR96110	Peptide provides s
31	14	70.0	5	18 AAW41637	Peptide used in de
32	14	70.0	5	18 AAW19714	Generic digestion
33	14	70.0	5	19 AAW69746	Digestion inhibit
34	14	70.0	5	19 AAW65835	Peptide #60 from p
35	14	70.0	5	20 AAY42926	Portion of the cor
36	14	70.0	5	20 AAY42927	Portion of the cor
37	14	70.0	5	20 AAY42928	Portion of the cor
38	14	70.0	5	20 AAY42929	Portion of the cor
39	14	70.0	5	21 AAB28349	Trypsin Modulating
40	14	70.0	5	21 AAB28350	Trypsin Modulating
41	14	70.0	5	21 AAB28353	Trypsin Modulating
42	14	70.0	5	21 AAB28354	Trypsin Modulating
43	14	70.0	5	21 AAB28356	Trypsin Modulating
44	14	70.0	5	21 AAB28357	Trypsin Modulating
45	14	70.0	5	21 AAB28363	Trypsin Modulating

ALIGNMENTS

RESULT 1
AAB37933
ID AAB37933 standard; peptide; 3 AA.
XX AAB37933;
AC AAB37933;
DT 27-FEB-2001 (first entry)
XX Trypsin modulating oostatic factor (TMOF) peptide SEQ ID 38.
DE Trypsin modulating oostatic factor (TMOF) peptide; pest control;
KW Trypsin modulating oostatic factor; TMOF; pesticide; pest control;
KW digestive enzyme synthesis inhibition; mosquito larvae; coleopterans;
KW lepidopteran; dipteran; blood-sucking insect; Diptera; *Nelima Locera*;
KW Colicidae; Culicinae; Corethrinae; Ceratopogonidae; Simuliidae.
XX Synthetic.
OS Synthetic.
XX WO2000063233-A2.
FN WO2000063233-A2.
XX 26-OCT-2000.
PD 26-OCT-2000.
XX 18-APR-2000; 2000WO-US10235.
PF 18-APR-1999; 99US-0295996.
XX 21-APR-1999;
PR (UYFL) UNIV FLORIDA RES FOUND INC.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX Borovsky D, Linderman RJ;
XX WPI; 2000-687156/67.
XX Novel trypsin modulating oostatic factor compound peptide useful for
PT pest control including pests of agricultural crops

XX
PS Claim 3; Page 33; 50pp; English.
XX
CC This invention relates to a trypsin modulating oostatic factor (TMOF)
CC compound. The compound specifically does not include the TMOF analogue
CC peptides represented by AAB37942 - AAB37949. Sequences AAB37900 -
CC AAB37941 are TMOF analogues which may be included in the composition. The
CC TMOF compound has pesticidal activity and is an inhibitor of pest
CC digestive enzyme synthesis. The TMOF compound is useful for controlling
CC pests such as mosquito larvae, coleopterans, lepidopterans, dipterans or
CC blood-sucking insects of order Diptera, suborder Nematocera, family
CC Colicidae or subfamily Culicinae, Corethrinae, Ceratopogonidae and
CC Simuliidae.
XX
SQ Sequence 3 AA;

Query Match 70.0%; Score 14; DB 21; Length 3;
Best Local Similarity 66.7%; Pred. No. 4.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
Db 1 pap 3

RESULT 2
AAR38441
ID AAR38441 standard; peptide; 4 AA.
XX
AC AAR38441;
XX
DT 04-NOV-1993 (first entry)
XX
DE Diuretic hormone binding peptide #2.
XX
DE Diuretic hormone; binding peptide; human; A type; reactivity; drugs;
KW binding affinity; detection; precursor; activation; modification.
XX
OS Synthetic.
XX
PN JP05132500-A.
XX
PD 28-MAY-1993.
XX
PF 11-NOV-1991; 91JP-0294295.
XX
PR 11-NOV-1991; 91JP-0294295.
XX
PA (HITB) HITACHI CHEM CO LTD.
XX
DR WPI; 1993-208849/26.
XX
PT New peptide with high binding affinity for diuretic hormone -
PT includes sequence of at least four aminoacid(s) complementary to
XX diuretic hormone, used in diagnosis
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC The sequences given in AAR38100 and AAR38441-69 are diuretic hormone
CC binding peptides. These peptides have sequences complementary to
CC human A type diuretic hormone. These peptides have specific
CC reactivity and high binding affinity to diuretic hormone. They are
CC useful for detecting agents to assay diuretic hormone or fragments
CC of it, eg. diuretic hormone precursor, and for activating or
XX modifying drugs.
XX
SQ Sequence 4 AA;

The sequences given in AAR38100 and AAR38441-69 are diuretic hormone
binding peptides. These peptides have sequences complementary to
CC human A type diuretic hormone. These peptides have specific
CC reactivity and high binding affinity to diuretic hormone. They are
CC useful for detecting agents to assay diuretic hormone or fragments
CC of it, eg. diuretic hormone precursor, and for activating or
XX modifying drugs.
XX
SQ Sequence 4 AA;

Query Match 70.0%; Score 14; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 4.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
Db 1 pap 3

RESULT 4
AAR38447
ID AAR38447 standard; peptide; 4 AA.
XX
AC AAR38447;
XX
DT 04-NOV-1993 (first entry)
XX
DE Diuretic hormone binding peptide #8.
XX
DE Diuretic hormone; binding peptide; human; A type; reactivity; drugs;
KW binding affinity; detection; precursor; activation; modification.
XX
OS Synthetic.

XX JP05132500-A.
PN
PD 28-MAY-1993.
XX PF 11-NOV-1991; 91JP-0294295.
XX PR 11-NOV-1991; 91JP-0294295.
XX PA (HITB) HITACHI CHEM CO LTD.
XX WPI; 1993-208849/26.
DR
PT New peptide with high binding affinity for diuretic hormone -
PT includes sequence of at least four aminoacid(s) complementary to
PT diuretic hormone, used in diagnosis
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC The sequences given in AAR38100 and AAR38441-69 are diuretic hormone
CC binding peptides. These peptides have sequences complementary to
CC human A type diuretic hormone. These peptides have specific
CC reactivity and high binding affinity to diuretic hormone. They are
CC useful for detecting agents to assay diuretic hormone or fragments
CC of it, eg. diuretic hormone precursor, and for activating or
CC modifying drugs.
XX
SQ Sequence 4 AA;

Query Match 70.0%; Score 14; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 4.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
Db | |
2 pap 4

RESULT 5
AAR38448
ID AAR38448 standard; peptide; 4 AA.
XX AC AAR38448;
XX
DT 04-NOV-1993 (first entry)
XX
DE Diuretic hormone binding peptide #9.
XX
KW Diuretic hormone; binding peptide; human; A type; reactivity; drugs;
KW binding affinity; detection; precursor; activation; modification.
XX
OS Synthetic.
XX
PN JP05132500-A.
XX
PD 28-MAY-1993.
XX
PF 11-NOV-1991; 91JP-0294295.
XX
PR 11-NOV-1991; 91JP-0294295.
XX
PA (HITB) HITACHI CHEM CO LTD.
XX
DR WPI; 1993-208849/26.
XX
PT New peptide with high binding affinity for diuretic hormone -
PT includes sequence of at least four aminoacid(s) complementary to
PT diuretic hormone, used in diagnosis
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC The sequences given in AAR38100 and AAR38441-69 are diuretic hormone

CC binding peptides. These peptides have sequences complementary to
CC human A type diuretic hormone. These peptides have specific
CC reactivity and high binding affinity to diuretic hormone. They are
CC useful for detecting agents to assay diuretic hormone or fragments
CC of it, eg. diuretic hormone precursor, and for activating or
CC modifying drugs.
XX
SQ Sequence 4 AA;

Query Match 70.0%; Score 14; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 4.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
Db | |
1 pap 3

RESULT 6
AAW58698
ID AAW58698 standard; peptide; 4 AA.
XX AC AAW58698;
XX
DT 09-SEP-1998 (first entry)
XX
DE Antigen epitope related to tumour lymph node metastasis peptide 2.
XX
KW Antigen epitope; tumour; lymph node; metastasis; cancer; BOY cell;
KW human; monoclonal antibody; ST-1; ST-2.
XX
OS Homo sapiens.
XX
PN JP10168098-A.
XX
PD 23-JUN-1998.
XX
PF 04-DEC-1996; 96JP-0340522.
XX
PR 04-DEC-1996; 96JP-0340522.
XX
PA (MEIP) MEIJI MILK PROD CO LTD.
PA (MURA/) MURAMATSU T.
XX
DR WPI; 1998-408687/35.
XX
PT New protein and peptide - useful for, e.g. elucidation of cancer
PT metastasis mechanism(s)
XX
PS Claim 1; Page 2; 20pp; Japanese.
XX
CC The present sequence represents a peptide whose sequence is found
CC in an antigen epitope related to tumour lymph node metastasis. The
CC present invention describes a protein or a peptide having an amino
CC acid sequence which is related to cancer metastasis. Also described
CC are: (1) DNA encoding the protein; (2) a vector containing the DNA;
CC (3) a transgenic host comprising the vector; (4) a monoclonal antibody
CC against the protein or the peptide, and (5) a monoclonal antibody
CC against an epitope related to tumour lymph node metastasis, and
CC containing Pro-Gly-Pro-Gly or Pro-Ala-Pro-Ala. The products may be
CC used for elucidation of mechanisms of metastasis of cancer.
XX
SQ Sequence 4 AA;

Query Match 70.0%; Score 14; DB 19; Length 4;
Best Local Similarity 66.7%; Pred. No. 4.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
Db | |
1 pap 3

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
 AAY33350
 ID AAY33350 standard; peptide; 4 AA.
 XX
 AC AAY33350;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Elastase inhibitor peptide fragment 2.
 XX
 KW Alpha-ketoester; alpha-ketoamide; acylated enol derivative; prodrug;
 KW elastase inhibitor; anti-inflammatory; antibacterial; antirheumatic;
 KW immunosuppressive; anticoagulant; antitumor; antithrombotic; emphysema;
 KW neutrophil-associated inflammatory disease; cystic fibrosis; septicemia;
 KW chronic obstructive pulmonary disease; gout; inflammatory bowel disease;
 KW adult respiratory distress syndrome; rheumatoid arthritis; bronchitis;
 KW disseminated intravascular coagulation.
 XX
 OS Synthetic.
 XX
 PN US5948886-A.
 XX
 PD 07-SEP-1999.
 XX
 PF 25-NOV-1997; 97US-0978096.
 XX
 PR 01-DEC-1996; 96US-0031083.
 XX
 PR 20-NOV-1996; 96US-0754081.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL INC.
 XX
 PI Mehdi S, Burkhardt JP, Peet NP;
 XX
 DR WPI; 1999-560023/47.
 XX
 PT Acylated enol derivatives of alpha-ketoester and alpha-ketoamide human
 PT neutrophil elastase inhibitors
 XX
 PS Example 6; Column 41-42; 25pp; English.
 XX
 CC This invention describes novel acylated enol derivatives of
 CC alpha-ketoesters and alpha-ketoamides, and their hydrates and salts. The
 CC products of the invention have anti-inflammatory, antibacterial,
 CC immunosuppressive, anticoagulant, antitumor, antithrombotic, and
 CC antithrombotic activity. The invention describes an in vitro assay of
 CC elastase in the presence of MDL 104569, performed using the chromogenic
 CC substrate N-MeOSuc-Ala-Ala-Pro-Val-p-nitroanilide. The assay mixture
 CC comprised partially purified elastase and substrate (0.2 mM) in 0.1 M
 CC HEPES (pH 7.5), 0.5M sodium chloride, 10 % dimethylsulfoxide and 0.1 %
 CC 'Brij 35' (RTM). The reaction (1 or 2 ml in a plastic cuvette) was
 CC maintained at 37°C and the hydrolysis of the substrate was followed in
 CC the presence of MDL 104569 and 5 units/ml of porcine liver esterase.
 CC Elastase was isolated from human sputum. The rate of hydrolysis of the
 CC substrate with no inhibitor or prodrug added was assigned as 100 %. In
 CC the presence of 1 mM MDL 104569, a rate of 81 % was obtained. When
 CC esterase (porcine kidney) was also present, the rate decreased to 24 %.
 CC At a concentration of 10 mM, the rate observed from the final extent
 CC of inhibition in the assay in the presence of esterase was 130 nM,
 CC compared to a K_i of 200 nM for the parent drug measured independently.
 CC The products of the invention are used to treat neutrophil-associated
 CC inflammatory diseases including emphysema, cystic fibrosis and chronic
 CC obstructive pulmonary disease as well as adult respiratory distress
 CC syndrome, septicemia, disseminated intravascular coagulation, gout,
 CC rheumatoid arthritis, chronic bronchitis and inflammatory bowel disease.
 CC This sequence represents a peptide used in the method of the invention.
 XX
 SQ Sequence 4 AA;

Query Match 70.0%; Score 14; DB 20; Length 4;
 Best Local Similarity 66.7%; Pred. No. 4.2e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PXP 4
 DB 1 ptp 3

Query Match 70.0%; Score 14; DB 20; Length 4;
 Best Local Similarity 66.7%; Pred. No. 4.2e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PXP 4
 DB 1 ptp 3

Sequence 4 AA;

WPI; 1999-508153/42.
 Non-crosslinked protein particles for therapeutic and diagnostic use
 Example 22; Column 107-108; 65pp; English.

This invention describes a novel aqueous suspension of monodisperse
 particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
 is stable against dissolving upon dilution with an alcohol-free aqueous
 medium. The method involves (a) forming an aqueous solution containing
 albumin and hemoglobin and (b) treating the aqueous solution with an
 alcohol to cause the solution to become turbid. The particles are useful
 as agents for in vivo administration, either of their own administration
 or as a vehicle for other therapeutic or diagnostic agents. The method
 permits the formation of albumin and hemoglobin particles in the
 nanometer and micrometer size range, in a form closer to their natural
 form than the forms of the prior art. The particles therefore constitute
 a more closely controlled agent for in vivo administration, with greater
 ease of clearance from the body after their period of usefulness.
 CC AAY30952-Y31135 represent peptides used in the method of the invention.

Sequence 4 AA;

KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW disseminated intravascular coagulation; rheumatoid arthritis.

RESULT 9

AAB74035
 ID AAB74035 standard; Peptide; 4 AA.

XX
 AC AAB74035;

XX
 DT 09-AUG-2001 (first entry)

XX Partial sequence contained in commercially available plasmid pmbac.

XX VEGF/PDGF-like factor; vascular endothelial growth factor; VEGF;
 KW platelet derived growth factor; PDGF; neovascularisation; disease.

XX Synthetic.

XX JP2001017188-A.

XX
 PD 23-JAN-2001.

XX
 PF 24-APR-2000; 2000JP-0122994.

XX
 PR 22-APR-1999; 99JP-0115516.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PA (HERI-) HERIKKUSU KENYUSHO KK.

XX WPI; 2001-285410/30.

XX New VEGF/PDGF-like factor useful for the development of treating agents
 PT for diseases accompanied by accentuation of abnormal neovascularization

XX Disclosure; Page 46; 52pp; Japanese.

XX The present sequence is provided in a specification relating
 CC to a novel vascular endothelial growth factor (VEGF)/platelet derived
 CC growth factor (PDGF)-like factor of 345 amino acids, or to a sequence
 CC in which at least one amino acid is deleted, replaced or added compared
 CC to the native sequence. The nucleotide sequence encoding the
 CC VEGF/PDGF-like factor may be integrated into a vector and used to
 CC transform a host cell. The VEGF/PDGF-like factor may be used in the
 CC development of agents for treating diseases associated with
 CC abnormal neovascularisation.

XX Sequence 4 AA;

Query Match 70.0%; Score 14; DB 22; Length 4;

Best Local Similarity 66.7%; Pred. No. 4.2e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 2 psp 4

RESULT 10

AAB46762
 ID AAB46762 standard; peptide; 4 AA.

XX
 AC AAB46762;

XX
 DT 18-APR-2001 (first entry)

XX L-prolinamide derived peptide fragment SEQ ID NO 7.

XX L-prolinamide; enol derivative; alpha-keto ester; alpha-keto amide;
 KW antiinflammatory; respiratory; antibacterial; anticoagulant; antigout;
 KW antiarthritic; gastrointestinal; prodrug; elastase inhibitor; gout;
 KW inflammatory disease; emphysema; cystic fibrosis; septicemia;
 KW chronic obstructive pulmonary disorder; chronic bronchitis;

OS Synthetic.
 XX US6172044-B1.

XX
 PD 09-JAN-2001.

XX
 PF 03-MAY-1999; 99US-0303965.

XX
 PR 01-DEC-1995; 95US-0031083.

XX
 PR 20-NOV-1996; 96US-0754081.

XX
 PR 25-NOV-1997; 97US-0978096.

XX (AVET) AVENTIS PHARM INC.

XX Peet NP, Burkhardt JP, Mehdi S;

XX WPI; 2001-201786/20.

XX New acylated enol derivatives of alpha-keto esters and alpha-keto
 PT amides used as prodrugs in treatment of e.g. emphysema and cystic
 PT fibrosis

XX Example 6; Column 39-40; 25pp; English.

XX This invention describes novel acylated enol derivatives (I) and (II) of
 CC alpha-keto esters and alpha-keto amides. The products of the invention
 CC have antiinflammatory, respiratory, antibacterial, anticoagulant,
 CC antigout, antiarthritic and gastrointestinal activity. The products of
 CC of the invention are used as prodrugs of known elastase inhibitors for
 CC treating inflammatory diseases, particularly emphysema, cystic fibrosis,
 CC chronic obstructive pulmonary disorder, adult respiratory distress
 CC syndrome, septicemia, disseminated intravascular coagulation, gout,
 CC rheumatoid arthritis, chronic bronchitis and inflammatory bowel disease.
 CC The compounds are used for treating guinea pigs, dogs, cats, rats, mice,
 CC horses, cattle and sheep.

XX Sequence 4 AA;

Query Match 70.0%; Score 14; DB 22; Length 4;

Best Local Similarity 66.7%; Pred. No. 4.2e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

Db 1 pap 3

RESULT 11

AAR29185
 ID AAR29185 standard; peptide; 5 AA.

XX
 AC AAR29185;

XX
 DT 13-APR-1993 (first entry)

XX Immunomodulatory thymopentin analogue #5.

XX Thymopentin; central nervous system; CNS; immune system; stress;
 KW anxiety; depression.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1

XX Modified-site 5 /note= "Acetyl-Arg"

XX Modified-site 5 /note= "Phe-NH2"

XX EP517464-A.

PN

XX 09-DEC-1992.
 XX
 XX 01-JUN-1992; 92EP-0305000.
 XX
 XX 03-JUN-1991; 91US-0708035.
 XX
 XX (IMMU-) IMMUNOBIOLOGY RES INST INC.
 XX
 XX Anwer MK, Audhya T, Goldstein G, Heavner G;
 XX WPI; 1992-408904/50.
 XX
 XX New penta:peptide derivs. enhance anti-CD3 stimulated T
 PT suppressor cell development - useful for treating the effects of
 PT ageing caused by shrinkage of the thymus and immune and central
 PT nervous system disorders
 XX
 XX Claim 4; Page 14; 2lpp; English.
 XX
 XX This peptide is a thymopentin analogue (Thymopentin is the active
 CC site of Thymopoietin and has the sequence Arg-Lys-Asp-Val-Tyr) with
 CC increased resistance to enzymatic degradation. The peptide has
 CC thymopoietin-like effects on the immune system and CNS; it is a
 CC potent immunomodulator and may be used to treat autoimmune diseases,
 CC age-related immune disorders, stress, anxiety and depression.
 XX
 XX Sequence 5 AA;

Query Match 70.0%; Score 14; DB 13; Length 5;
 Best Local Similarity 66.7%; Pred. No. 4.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 2 pap 4

RESULT 12
 AAR29186
 ID AAR29186 standard; peptide; 5 AA.
 AC AAR29186;
 XX
 XX 13-APR-1993 (first entry)
 XX
 XX Immunomodulatory Thymopentin analogue #6.
 DE
 XX Thymopoietin; central nervous system; CNS; immune system; stress;
 KW anxiety; depression.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "Acetyl-Arg"
 FT Modified-site 5
 FT /note= "Tyr-NH2"
 XX
 XX EP517464-A.
 PN
 XX 09-DEC-1992.
 XX
 XX 01-JUN-1992; 92EP-0305000.
 XX
 XX 03-JUN-1991; 91US-0708035.
 XX
 XX (IMMU-) IMMUNOBIOLOGY RES INST INC.
 XX
 XX Anwer MK, Audhya T, Goldstein G, Heavner G;
 XX WPI; 1992-408904/50.

XX New penta:peptide derivs. enhance anti-CD3 stimulated
 PT suppressor cell development - useful for treating the effects of
 PT ageing caused by shrinkage of the thymus and immune and central
 PT nervous system disorders
 XX
 XX Claim 4; Page 14; 2lpp; English.
 XX
 XX This peptide is a thymopentin analogue (Thymopentin is the active
 CC site of Thymopoietin and has the sequence Arg-Lys-Asp-Val-Tyr) with
 CC increased resistance to enzymatic degradation. The peptide has
 CC thymopoietin-like effects on the immune system and CNS; it is a
 CC potent immunomodulator and may be used to treat autoimmune diseases,
 CC age-related immune disorders, stress, anxiety and depression.
 XX
 XX Sequence 5 AA;

Query Match 70.0%; Score 14; DB 13; Length 5;
 Best Local Similarity 66.7%; Pred. No. 4.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 2 pap 4

RESULT 13
 AAR29188
 ID AAR29188 standard; peptide; 5 AA.
 XX
 XX AAR29188;
 XX
 XX 13-APR-1993 (first entry)
 XX
 XX Immunomodulatory Thymopentin analogue #8.
 DE
 XX Thymopoietin; central nervous system; CNS; immune system; stress;
 KW anxiety; depression.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "Acetyl-Arg"
 FT Modified-site 5
 FT /note= "Phe-NH2"
 XX
 XX EP517464-A.
 PN
 XX 09-DEC-1992.
 XX
 XX 01-JUN-1992; 92EP-0305000.
 XX
 XX 03-JUN-1991; 91US-0708035.
 XX
 XX (IMMU-) IMMUNOBIOLOGY RES INST INC.
 XX
 XX Anwer MK, Audhya T, Goldstein G, Heavner G;
 XX WPI; 1992-408904/50.
 XX
 XX New penta:peptide derivs. enhance anti-CD3 stimulated T
 PT suppressor cell development - useful for treating the effects of
 PT ageing caused by shrinkage of the thymus and immune and central
 PT nervous system disorders
 XX
 XX Claim 4; Page 14; 2lpp; English.
 XX
 XX This peptide is a thymopentin analogue (Thymopentin is the active
 CC site of Thymopoietin and has the sequence Arg-Lys-Asp-Val-Tyr) with
 CC increased resistance to enzymatic degradation. The peptide has
 CC thymopoietin-like effects on the immune system and CNS; it is a

CC potent immunomodulator and may be used to treat autoimmune diseases,
 XX age-related immune disorders, stress, anxiety and depression.
 SQ Sequence 5 AA;

Query Match 70.0%; Score 14; DB 13; Length 5;
 Best Local Similarity 66.7%; Pred. No. 4.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |
 Db 2 psp 4

RESULT 14

AAR29189
 ID AAR29189 standard; peptide; 5 AA.

XX AC AAR29189;

XX DT 13-APR-1993 (first entry)

XX DE Immunomodulatory Thymopentin analogue #9.

XX KW Thymopietin; central nervous system; CNS; immune system; stress;
 XX KW anxiety; depression.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Acetyl-Arg"

FT Modified-site 5

FT /note= "Phe-NH2"

XX PN EP517464-A.

XX PD 09-DEC-1992.

XX PF 01-JUN-1992; 92EP-0305000.

XX PR 03-JUN-1991; 91US-0708035.

XX PA (IMMU-) IMMUNOBIOLOGY RES INST INC.

XX PI Anwer MK, Audhya T, Goldstein G, Heavner G;

XX DR WPI; 1992-408904/50.

XX PT New penta:peptide derivs. enhance anti-CD3 stimulated T
 PT suppressor cell development - useful for treating the effects of
 PT ageing caused by shrinkage of the thymus and immune and central
 PT nervous system disorders

XX PS Claim 4; Page 14; 2lpp; English.

XX CC This peptide is a thymopentin analogue (Thymopentin is the active
 CC site of Thymopietin and has the sequence Arg-Lys-Asp-Val-Tyr) with
 CC increased resistance to enzymatic degradation. The peptide has
 CC thymopietin-like effects on the immune system and CNS; it is a
 CC potent immunomodulator and may be used to treat autoimmune diseases,
 CC age-related immune disorders, stress, anxiety and depression.

XX SQ Sequence 5 AA;

Query Match 70.0%; Score 14; DB 13; Length 5;
 Best Local Similarity 66.7%; Pred. No. 4.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4
 | |

Db 2 ptp 4

RESULT 15

AAR29190
 ID AAR29190 standard; peptide; 5 AA.

XX AC AAR29190;

XX DT 13-APR-1993 (first entry)

XX DE Immunomodulatory Thymopentin analogue #10.

XX KW Thymopietin; central nervous system; CNS; immune system; stress;
 XX KW anxiety; depression.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Acetyl-Arg"

FT Modified-site 5

FT /note= "Tyr-NH2"

XX PN EP517464-A.

XX PD 09-DEC-1992.

XX PF 01-JUN-1992; 92EP-0305000.

XX PR 03-JUN-1991; 91US-0708035.

XX PA (IMMU-) IMMUNOBIOLOGY RES INST INC.

XX PI Anwer MK, Audhya T, Goldstein G, Heavner G;

XX DR WPI; 1992-408904/50.

XX PT New penta:peptide derivs. enhance anti-CD3 stimulated T
 PT suppressor cell development - useful for treating the effects of
 PT ageing caused by shrinkage of the thymus and immune and central
 PT nervous system disorders

XX PS Claim 4; Page 14; 2lpp; English.

XX CC This peptide is a thymopentin analogue (Thymopentin is the active
 CC site of Thymopietin and has the sequence Arg-Lys-Asp-Val-Tyr) with
 CC increased resistance to enzymatic degradation. The peptide has
 CC thymopietin-like effects on the immune system and CNS; it is a
 CC potent immunomodulator and may be used to treat autoimmune diseases,
 CC age-related immune disorders, stress, anxiety and depression.

XX SQ Sequence 5 AA;

Query Match 70.0%; Score 14; DB 13; Length 5;
 Best Local Similarity 66.7%; Pred. No. 4.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PXP 4

| |

Db 2 ptp 4

Search completed: March 15, 2002, 14:22:28
 Job time: 368 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:31:51 ; Search time 48.07 Seconds
(without alignments)
14.595 Million cell updates/sec

Title: US-09-988-792-2

Perfect score: 71

Sequence: 1 RPKPQQWFWM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 302707 seqs, 63781257 residues

Total number of hits satisfying chosen parameters: 302707

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	71	100.0	11	US-09-988-792-2	Sequence 2, Appli
2	48	67.6	11	US-09-988-792-1	Sequence 1, Appli
3	48	67.6	11	US-09-988-792-7	Sequence 7, Appli
4	48	67.6	11	US-09-570-022-1	Sequence 1, Appli
5	48	67.6	11	US-10-002-593-4	Sequence 4, Appli
6	48	67.6	11	US-10-053-669-3	Sequence 3, Appli
7	48	67.6	12	US-09-489-667B-2	Sequence 2, Appli
8	48	67.6	12	US-09-489-667B-5	Sequence 5, Appli
9	48	67.6	12	US-09-489-667B-8	Sequence 8, Appli
10	48	67.6	12	US-10-050-200-55	Sequence 55, Appli
11	48	67.6	13	US-09-489-667B-3	Sequence 3, Appli
12	48	67.6	13	US-09-489-667B-6	Sequence 6, Appli
13	48	67.6	13	US-09-489-667B-9	Sequence 9, Appli
14	48	67.6	14	US-09-489-667B-4	Sequence 4, Appli
15	48	67.6	14	US-09-489-667B-7	Sequence 7, Appli
16	48	67.6	14	US-09-489-667B-10	Sequence 10, Appli
17	48	67.6	20	US-09-570-022-23	Sequence 23, Appli
18	45	63.4	11	US-09-988-792-8	Sequence 8, Appli
19	44	62.0	36	US-09-620-394B-916	Sequence 916, App
20	43	60.6	11	US-09-489-667B-1	Sequence 1, Appli
21	43	60.6	11	US-09-988-792-13	Sequence 13, Appli
22	43	60.6	11	US-09-935-682-64	Sequence 64, Appli
23	42	59.2	193	US-09-826-734-160	Sequence 160, App
24	42	59.2	264	US-09-675-784A-10875	Sequence 10875, A
25	41	57.7	9	US-09-489-667B-13	Sequence 13, Appli

26	41	57.7	142	6	US-09-708-427-57514	Sequence 57514, A
27	40	56.3	11	6	US-09-570-022-5	Sequence 5, Appli
28	40	56.3	45	6	US-09-614-150-30975	Sequence 30975, A
29	40	56.3	90	6	US-09-708-427-62158	Sequence 62158, A
30	40	56.3	106	6	US-09-845-849-8	Sequence 8, Appli
31	40	56.3	285	6	US-09-620-394B-3530	Sequence 3530, Ap
32	40	56.3	288	6	US-09-675-784A-12622	Sequence 12622, A
33	40	56.3	289	6	US-09-708-427-13324	Sequence 13324, A
34	40	56.3	317	6	US-09-620-394B-3529	Sequence 3529, Ap
35	40	56.3	321	6	US-09-708-427-13323	Sequence 13323, A
36	40	56.3	363	6	US-09-688-072-39	Sequence 39, Appli
37	40	56.3	367	6	US-09-620-394B-3528	Sequence 3528, Ap
38	40	56.3	371	6	US-09-708-427-13322	Sequence 13322, A
39	40	56.3	381	6	US-60-356-051-1651	Sequence 1651, Ap
40	40	56.3	411	6	US-09-980-350-2	Sequence 2, Appli
41	40	56.3	411	7	US-10-036-657-36	Sequence 36, Appli
42	40	56.3	411	7	US-10-036-657-38	Sequence 38, Appli
43	40	56.3	426	4	US-08-816-011E-45	Sequence 45, Appli
44	40	56.3	426	4	US-08-816-011F-45	Sequence 45, Appli
45	40	56.3	665	6	US-09-614-150-17271	Sequence 17271, A

ALIGNMENTS

RESULT 1

US-09-988-792-2
; Sequence 2, Application US/09988792
; GENERAL INFORMATION:
; APPLICANT: Lipkowski, Andrezej W
; APPLICANT: Carr, Daniel B
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: 18475-025
; CURRENT APPLICATION NUMBER: US/09/988,792
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,369
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)
; OTHER INFORMATION: Wherein Pro is D-proline
; NAME/KEY: VARIANT
; LOCATION: (7)
; OTHER INFORMATION: Wherein Trp is D-tryptophan
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: Wherein Trp is D-tryptophan
US-09-988-792-2

Query Match 100.0%; Score 71; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9,5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11

Db 1 RPKPQQWFWM 11

RESULT 2

US-09-988-792-1
; Sequence 1, Application US/09988792
; GENERAL INFORMATION:
; APPLICANT: Lipkowski, Andrezej W
; APPLICANT: Carr, Daniel B
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: 18475-025

; CURRENT APPLICATION NUMBER: US/09/988,792
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,369
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-988-792-1

Query Match 67.6%; Score 48; DB 6; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.24; Mismatches 1; Indels 1; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | |
Db 1 RPKPQQFFGLM 11

RESULT 3
US-09-988-792-7
; Sequence 7, Application US/09988792
; GENERAL INFORMATION:
; APPLICANT: Lipkowski, Andrezej W
; APPLICANT: Carr, Daniel B
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: 18475-025
; CURRENT APPLICATION NUMBER: US/09/988,792
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,369
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-09-988-792-7

Query Match 67.6%; Score 48; DB 6; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.24; Mismatches 1; Indels 1; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | |
Db 1 RPKPQQFFGLM 11

RESULT 4
US-09-570-022-1
; Sequence 1, Application US/09570022
; GENERAL INFORMATION:
; APPLICANT: GORDON, RICHARD K.
; APPLICANT: MOORAD, DEBORAH R.
; APPLICANT: DOCTOR, BHUPENDRA P.
; APPLICANT: GARCIA, GREGORY E.
; TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
; FILE REFERENCE: 38644-170531
; CURRENT APPLICATION NUMBER: US/09/570,022
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,446
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-570-022-1

Query Match 67.6%; Score 48; DB 6; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.24; Mismatches 1; Indels 1; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | |
Db 1 RPKPQQFFGLM 11

RESULT 5
US-10-002-593-4
; Sequence 4, Application US/10002593
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Brown, Nancy J.
; TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTING ENZYME INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA
; FILE REFERENCE: Atty Docket No. 1242/48/2
; CURRENT APPLICATION NUMBER: US/10/002,593
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/244,524
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-593-4

Query Match 67.6%; Score 48; DB 7; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.24; Mismatches 1; Indels 1; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | : | |
Db 1 RPKPQQFFGLM 11

RESULT 6
US-10-053-669-3
; Sequence 3, Application US/10053669
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
; FILE REFERENCE: NI427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD_RES
; LOCATION: (11)..(11)
; OTHER INFORMATION: AMIDATION
US-10-053-669-3

Query Match 67.6%; Score 48; DB 7; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.24; Mismatches 1; Indels 1; Gaps 0;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11

Db 1 RPKPQQFFGLM 11
|||||:| |

RESULT 7

US-09-489-667B-2

; Sequence 2, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Precursor to substance P, which is very well known in the art.
US-09-489-667B-2

Query Match 67.6%; Score 48; DB 6; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.27;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||:| |
Db 1 RPKPQQFFGLM 11

RESULT 8

US-09-489-667B-5

; Sequence 5, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester synthetase precursor to substance P.
; NAME/KEY: MISC_FEATURE
; LOCATION: (12)..(12)
; OTHER INFORMATION: Xaa at position 12 is Glycine Methyl Ester
US-09-489-667B-5

Query Match 67.6%; Score 48; DB 6; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.27;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||:| |
Db 1 RPKPQQFFGLM 11

RESULT 9

US-09-489-667B-8

; Sequence 8, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain

; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester synthetase precursor to substance P.
; NAME/KEY: MISC_FEATURE
; LOCATION: (12)..(12)
; OTHER INFORMATION: Xaa at position 12 is Glycine Ethyl Ester
US-09-489-667B-8

Query Match 67.6%; Score 48; DB 6; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.27;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||:| |
Db 1 RPKPQQFFGLM 11

RESULT 10

US-10-050-200-55
; Sequence 55, Application US/10050200
; GENERAL INFORMATION:
; APPLICANT: Fourie, Anne
; APPLICANT: Coles, Fawn
; APPLICANT: Karlsson, Lars
; TITLE OF INVENTION: Aggrecanase-1 and -2 Peptide Substrates and Methods
; FILE REFERENCE: ORT-1417
; CURRENT APPLICATION NUMBER: US/10/050,200
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide substrate
US-10-050-200-55

Query Match 67.6%; Score 48; DB 7; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.27;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
|||||:| |
Db 2 RPKPQQFFGLM 12

RESULT 11

US-09-489-667B-3
; Sequence 3, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown

;
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a precursor to substance
; OTHER INFORMATION: e p and is very well known in the art.
US-09-489-667B-3

Query Match 67.6%; Score 48; DB 6; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.29;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
| | | | | | | | | |
Db 1 RPKPQQFFGLM 11

RESULT 12
US-09-489-667B-6
; Sequence 6, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester synt
; NAME/KEY: MISC.FEATURE
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa at position 13 is Lysine Methyl Ester
US-09-489-667B-6

Query Match 67.6%; Score 48; DB 6; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.29;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
| | | | | | | | | |
Db 1 RPKPQQFFGLM 11

RESULT 13
US-09-489-667B-9
; Sequence 9, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester synt
; NAME/KEY: MISC.FEATURE
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa at position 13 is Lysine Ethyl Ester
US-09-489-667B-9

Query Match 67.6%; Score 48; DB 6; Length 13;

Best Local Similarity 81.8%; Pred. No. 0.29;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
| | | | | | | | | |
Db 1 RPKPQQFFGLM 11

RESULT 14
US-09-489-667B-4
; Sequence 4, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This is a precursor to subst
; OTHER INFORMATION: e p and is very well known in the art.
US-09-489-667B-4

Query Match 67.6%; Score 48; DB 6; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.31;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
| | | | | | | | | |
Db 1 RPKPQQFFGLM 11

RESULT 15
US-09-489-667B-7
; Sequence 7, Application US/09489667B
; GENERAL INFORMATION:
; APPLICANT: Donovan, Stephen
; TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
; FILE REFERENCE: D-2875
; CURRENT APPLICATION NUMBER: US/09/489,667B
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This is a carboxy-ester s
; NAME/KEY: MISC.FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa at position 14 is Arginine Methyl Ester
US-09-489-667B-7

Query Match 67.6%; Score 48; DB 6; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.31;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
| | | | | | | | | |
Db 1 RPKPQQFFGLM 11

Search completed: March 15, 2002, 14:31:52

Job time: 561 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:30:57 ; Search time 63.84 Seconds
(without alignments)
25.204 Million cell updates/sec

Title: US-09-988-792-2

Perfect score: 71

Sequence: 1 RPKPQOWFWLM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organella:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	67.6	72	4	Q9Y494
2	48	67.6	114	6	Q97947
3	48	67.6	128	4	Q9Y6V5
4	48	67.6	129	6	Q97948
5	45	63.4	453	2	Q9PL30
6	45	63.4	455	2	O84013
7	44	62.0	97	11	Q9Z0K2
8	44	62.0	115	11	Q9Z0K1
9	44	62.0	130	11	Q9Z0K0
10	43	60.6	314	2	Q9A645
11	43	60.6	365	2	Q9JY60
12	43	60.6	365	2	Q9JY60
13	43	60.6	818	12	Q9PWS3
14	43	60.6	898	12	Q9PYP2
15	41	57.7	158	2	O34889
16	41	57.7	159	2	O84560
17	41	57.7	209	11	Q9DAS6
18	41	57.7	261	2	Q9HXA6
19	41	57.7	286	2	Q9PAV0

20	41	57.7	290	2	Q9AKK5
21	41	57.7	291	2	Q55507
22	41	57.7	304	1	Q9HNN1
23	41	57.7	392	2	Q9F849
24	41	57.7	529	2	P74332
25	40	56.3	45	5	Q9V6W6
26	40	56.3	154	11	Q9R129
27	40	56.3	155	11	Q9R132
28	40	56.3	155	11	Q9R131
29	40	56.3	155	11	Q9R127
30	40	56.3	155	11	Q9JKI6
31	40	56.3	273	2	Q9KRQ9
32	40	56.3	289	2	Q9JYV2
33	40	56.3	289	2	Q9JYV2
34	40	56.3	290	2	Q9JYV2
35	40	56.3	290	2	Q9JYV2
36	40	56.3	290	2	Q9AKF0
37	40	56.3	290	2	Q9AKA6
38	40	56.3	318	2	Q9KVD3
39	40	56.3	332	2	O82937
40	40	56.3	343	2	Q9ZG03
41	40	56.3	363	2	P73727
42	40	56.3	367	10	Q9C5G0
43	40	56.3	381	10	Q9FY15
44	40	56.3	411	4	Q9NRT2
45	40	56.3	639	4	Q9H8K3
46	40	56.3	665	5	Q9V7L5

ALIGNMENTS

RESULT 1
Q9Y494 PRELIMINARY; PRT; 72 AA.
AC Q9Y494
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=BLOOD, AND BRAIN;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT Identification of a Delta isoform of preprotachykinin mRNA in Human
RL Mononuclear Phagocytes and Lymphocytes."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050657; AAC15703.1;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
FT SMART; SM00203; TK; 2.
FT NON_TER 1 1
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 8274 MW; 2C02B2BA41EAAD16 CRC64;

Query Match 67.6%; Score 48; DB 4; Length 7;
Best Local Similarity 81.8%; Pred. No. 1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 RPKPQOWFWLM 11
|||||:|
Db 23 RPKPQOWFWLM 33

RESULT 2
Q97947 PRELIMINARY; PRT; 114 AA.
ID Q97947

```

AC O97947;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ I.
OS Tupaia belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50785; CAA90648.1;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 83 92 NEUROKININ A.
SQ SEQUENCE 114 AA; 13281 MW; B439C3D27FD47CAB CRC64;

Query Match 67.6%; Score 48; DB 6; Length 114;
Best Local Similarity 81.8%; Pred. No. 1.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
DB 58 RPKPQQFFGLM 68
|||||:|

RESULT 3
QY6V5
ID QY6V5 PRELIMINARY; PRT; 128 AA.
AC QY6V5;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE WUGSC:H-DJ0841B21.1 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kalicki J., Angell S.;
RT "The sequence of Homo sapiens PAC clone DJ0841B21.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004140; AAC02754.1;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 1.
SQ SEQUENCE 128 AA; 14770 MW; 0F8D61774AFEC1CA CRC64;

Query Match 67.6%; Score 48; DB 4; Length 128;
Best Local Similarity 81.8%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|

```

```

DB 58 RPKPQQFFGLM 68

RESULT 4
O97948
ID O97948 PRELIMINARY; PRT; 129 AA.
AC O97948;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Tupaia belangeri (northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50786; CAA90649.1;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR ProDom; PD005598; Protachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 129 AA; 14941 MW; 5855E7ADC2D8674E CRC64;

Query Match 67.6%; Score 48; DB 6; Length 129;
Best Local Similarity 81.8%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
|||||:|
DB 58 RPKPQQFFGLM 68

RESULT 5
O9PL30
ID O9PL30 PRELIMINARY; PRT; 453 AA.
AC O9PL30;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE, PUTATIVE.
GN TC0278.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOPN / NIGG;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Otterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002295; AAF39146.1;
DR TIGR; TC0278;
KW Complete proteome.
SQ SEQUENCE 453 AA; 51463 MW; 6221515A00A093FF CRC64;

```

Query Match 63.4%; Score 45; DB 2; Length 453;
Best Local Similarity 75.0%; Pred. NO. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
II:III II
DB 303 KPEQWLWL 310

RESULT 6
O84013 PRELIMINARY; PRT; 455 AA.
AC O84013;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ACYLTRANSFERASE.
GN HTRB OR CT010.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UV-3/CX;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammell C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
DR EMBL; AF001275; AAC67600.1; -;
KW Transferase; Acyltransferase; Complete proteome.
SQ SEQUENCE 455 AA; 52058 MW; 0404B6326C67ACCF CRC64;

Query Match 63.4%; Score 45; DB 2; Length 455;
Best Local Similarity 75.0%; Pred. NO. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQWFWL 10
II:III II
DB 303 KPEQWLWL 310

RESULT 7
O920K2 PRELIMINARY; PRT; 97 AA.
AC O920K2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DELTA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50782; CAA90645.1; -;
DR InterPro: IPRO03580; Protachykinin.
DR ProDom: PD005598; Protachykinin; I.
FT CHAIN 58 68 SUBSTANCE P.
SQ SEQUENCE 97 AA; 11222 MW; FFD50C3297E3F7E3 CRC64;

Query Match 62.0%; Score 44; DB 11; Length 97;
Best Local Similarity 81.8%; Pred. NO. 5.7;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWLM 11
IIIIII II
DB 58 RPKPQQSFGLM 68

RESULT 8
Q920K1 PRELIMINARY; PRT; 115 AA.
AC Q920K1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50783; CAA90646.1; -;
DR InterPro: IPRO02040; Tachykinin.
DR ProDom: PD005598; Protachykinin; I.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 92 NEUROPEPTIDE GAMMA.
FT CHAIN 83 92 NEUROKININ A.
SQ SEQUENCE 115 AA; 13190 MW; 39EFFB8CB47174 CRC64;

Query Match 62.0%; Score 44; DB 11; Length 111;
Best Local Similarity 81.8%; Pred. NO. 6.7;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPQQWFWLM 11
IIIIII II
DB 58 RPKPQQSFGLM 68

RESULT 9
Q920K0 PRELIMINARY; PRT; 130 AA.
AC Q920K0;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BETA PREPROTACHYKININ I.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIRBRIDGE WHITE; TISSUE=BRAIN;
RA Heitland A., Maegert H.J., Kruhoffer M., Forssmann W.G.;
RT "Tachykinin precursors are highly conserved among different mammals.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50784; CAA90647.1; -;
DR InterPro: IPRO02040; Tachykinin.
DR InterPro: IPRO03580; Protachykinin.
DR ProDom: PD005598; Protachykinin; I.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
FT CHAIN 58 68 SUBSTANCE P.
FT CHAIN 72 107 NEUROPEPTIDE K.
FT CHAIN 98 107 NEUROKININ A.
SQ SEQUENCE 130 AA; 14850 MW; C4B2F5B6A60A7C0 CRC64;

Query Match 62.0%; Score 44; DB 11; Length 130;
 Best Local Similarity 81.8%; Pred. No. 7.6;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFWFLM 11
 ||||| | |
 DB 58 RPKPOQSFGLM 68

RESULT 10

Q9A645 PRELIMINARY; PRT; 314 AA.
 AC Q9A645;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE HYPOTHETICAL PROTEIN CC2250.
 GN CC2250.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCBI_TaxID=69394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21173698; PubMed=11259647;
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005895; AAK24221.1; -;
 DR TIGR; CC2250; -;
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 314 AA; 35316 MW; 59825ADE764362A CRC64;

Query Match 60.6%; Score 43; DB 2; Length 314;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFWFLM 10
 | | | | |
 DB 282 RRPFAEWFV 291

RESULT 11

Q9JY60 PRELIMINARY; PRT; 365 AA.
 AC Q9JY60;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE, SUBUNIT III.
 GN NMB1723.
 OS *Neisseria meningitidis* (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58."
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002522; AAF42068.1; -;
 DR TIGR; NMB1723; -;
 DR InterPro; IPR000345; CytC_heme_bind.
 DR InterPro; IPR003088; Cyt_C1.
 DR InterPro; IPR002329; Cyt_C1C.
 DR Pfam; PF00034; cytochrome_c_2.
 DR PRINTS; PR00605; CYTOCHROME_C.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 365 AA; 40039 MW; AF344435A51EB4A2 CRC64;

Query Match 60.6%; Score 43; DB 2; Length 365;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQFWFLM 10
 | | | | |
 DB 62 PLPRWFWFL 70

RESULT 12

Q9JT44 PRELIMINARY; PRT; 365 AA.
 AC Q9JT44;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PUTATIVE CYTOCHROME C.
 GN NMA1977.
 OS *Neisseria meningitidis* (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE=2022556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491."
 RL Nature 404:502-506(2000).
 DR EMBL; AL162757; CAB85197.1; -;
 DR InterPro; IPR000345; CytC_heme_bind.
 DR InterPro; IPR003088; Cyt_C1.
 DR InterPro; IPR002329; Cyt_C1C.
 DR Pfam; PF00034; cytochrome_c_2.
 DR PRINTS; PR00605; CYTOCHROME_C.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 365 AA; 40011 MW; AF223552A51EB4A2 CRC64;

Query Match 60.6%; Score 43; DB 2; Length 365;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQFWFLM 10
 | | | | |
 DB 62 PLPRWFWFL 70

RESULT 13

Q9PWS3 PRELIMINARY; PRT; 818 AA.
 ID Q9PWS3
 AC Q9PWS3;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE GAG-ABL PROTEIN (FRAGMENT)
 OS Abelson murine leukemia virus
 OC Viruses; Retroviral viruses; Retroviridae; Mammalian type C retroviruses.
 OX NCBI_TaxID=11788;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Lee R., Paskind M., Wang J.Y.J., Baltimore D.;
 RT "Abelson (P160) murine leukemia virus (Ab-MLV) abl gene.";
 RL (In) Weiss R., Teich N., Varmus H., Coffin J. (eds.);
 RL RNA tumor viruses, pp.861-868, Cold Spring Harbor Laboratory Press,
 RL New York (1985).
 DR EMBL; X02963; CAB56204.1; .
 DR HSSP; P00519; 2ABL.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001245; Tyr_kin.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00001; SH2; 1.
 KW ATP-binding; transferase; Tyrosine-protein kinase.
 FT NON_TER
 FT SEQUENCE 818 AA; 90973 MW; C2F5F417D0A9F50C CRC64;

Query Match 60.6%; Score 43; DB 12; Length 818;
 Best Local Similarity 77.8%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQOWFWL 10
 II III II
 Db 545 PKGQWGWL 553

RESULT 14
 ID Q9PY2 PRELIMINARY; PRT; 898 AA.
 AC Q9PY2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE ORF154.
 DE ORF154.
 GN ORF154.
 OS Xestia c-nigrum granulosis virus (Xngv) (Xestia c-nigrum
 OS granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OX NCBI_TaxID=51677;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA MEDLINE-99434230; PubMed-10502508;
 RA Hayakawa T., Ko R., Okano K., Seong S.I., Goto C., Maeda S.;
 RT "Sequence analysis of the Xestia c-nigrum granulovirus genome."
 RL Virology 262:277-297(1999).
 DR EMBL; AF162221; AAF05268.1; .
 DR SEQUENCE 898 AA; 104261 MW; DDE9900AEE146834 CRC64;

Query Match 60.6%; Score 43; DB 12; Length 898;
 Best Local Similarity 70.0%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQOWFWL 11
 I III III
 Db 353 PYQIWAFLM 362

RESULT 15
 ID Q34889 PRELIMINARY; PRT; 158 AA.
 AC Q34889;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 18.7 KDA PROTEIN YVAV (ORFA).
 GN YVAV.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=JH642;
 RC Nakamura A., Grau R., Perego M., Hoch J.A.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Chai S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallon N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Jorba B., Karamata D., Kasahara Y., Klier-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinot S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis."
 RL Nature 390:249-256(1997).
 DR EMBL; AB006738; BAA21900.1; .
 DR EMBL; Z99121; CAB15380.1; .
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 158 AA; 18650 MW; C495D20D39CF46C7 CRC64;

Query Match 57.7%; Score 41; DB 2; Length 158;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPQOWFWL 10
 I III I
 Db 131 RQPLSWYWI 140

Search completed: March 15, 2002, 14:30:59
 Job time: 578 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:32:18 ; Search time 20.4 Seconds
(without alignments)
19.770 Million cell updates/sec

Title: US-09-988-792-2

Perfect score: 71

Sequence: 1 RPKPQWFWM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	67.6	11	1 TKNA_HORSE	P01290 equus cabal
2	48	67.6	115	1 TKNI_RABIT	P41540 corytolagus
3	48	67.6	129	1 TKNI_HUMAN	P20366 homo sapien
4	48	67.6	130	1 TKNI_BOVIN	P01289 bos taurus
5	48	67.6	130	1 TKNI_MESAU	Q60541 mesocricetu
6	48	67.6	130	1 TKNI_MOUSE	P41539 mus musculus
7	48	67.6	130	1 TKNI_RAT	P06767 rattus norv
8	45	63.4	11	1 TKNA_CHICK	P19850 gallus gall
9	44	62.0	436	1 CYB_RHOCA	P08502 rhodobacter
10	43	60.6	902	1 VEF_GVHA	P54232 heliothis a
11	42	59.2	377	1 DCHS_ENTAE	P28577 enterobacte
12	41	57.7	55	1 ATP8_SOUAC	Q92250 squalus aca
13	40	56.3	411	1 CIW2_MOUSE	P97438 mus musculu
14	40	56.3	426	1 CIW2_MOUSE	Q95069 homo sapien
15	40	56.3	538	1 CIWA_HUMAN	P57789 homo sapien
16	40	56.3	538	1 CIWA_RAT	Q97434 rattus norv
17	40	56.3	665	1 CNG_DROME	Q24278 drosophila
18	39	54.9	361	1 FUT3_HUMAN	P21217 homo sapien
19	39	54.9	372	1 FUT3_PANTR	Q19058 pan troglod
20	39	54.9	374	1 FUT5_HUMAN	Q11128 homo sapien
21	39	54.9	374	1 FUT5_PANTR	P56433 pan troglod
22	39	54.9	440	1 CYB_PARDE	P05418 paracoccus
23	39	54.9	816	1 NPA2_MOUSE	P97460 mus musculu
24	39	54.9	824	1 NPA2_HUMAN	Q99743 homo sapien
25	39	54.9	846	1 CLOC_HUMAN	O15516 homo sapien
26	39	54.9	855	1 CLOC_MOUSE	O08785 mus musculu
27	39	54.9	1023	1 CLOC_DROME	O61735 drosophila
28	38	53.5	323	1 MSBB_ECOLI	P24205 escherichia
29	38	53.5	330	1 LSP1_MOUSE	P19973 mus musculu
30	38	53.5	405	1 FUT4_HUMAN	P22083 homo sapien
31	38	53.5	433	1 FUT4_MOUSE	Q11127 mus musculu
32	38	53.5	433	1 FUT4_RAT	Q62994 rattus norv
33	38	53.5	533	1 YADC_SCHPO	Q09837 schizosacch

ALIGNMENTS

RESULT 1

TKNA_HORSE
ID TKNA_HORSE STANDARD; PRT; 11 AA.
AC P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE SUBSTANCE P.
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS Equus caballus (Horse), and Cavia porcellus (Guinea pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796, 10141;
RN [1]
RP SEQUENCE.
RC SPECIES=Horse;
RA Studer R.O., Trzeciak A., Lergier W.;
RT "Isolation and amino-acid sequence of substance P from horse
intestine.";
RL Helv. Chim. Acta 56:860-866(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C. porcellus;
RX MEDLINE=90044895; PubMed=2478925;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P.";
RL Neuropeptides 14:105-110(1989).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01558; SPHO.
DR PIR; A60654; A60654.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuroptide; Amidation; Neurotransmitter.
FT MOD_RES 11
FT AMIDATION
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C67 CRC64;

Query Match 67.6%; Score 48; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.17;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQWFWM 11

|||||:|

Db 1 RPKPQWFWM 11

RESULT 2

TKNI_RABIT
ID TKNI_RABIT STANDARD; PRT; 115 AA.

P41540;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ I PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE GAMMA; C-TERMINAL
 DE FLANKING PEPTIDE].
 DE TAC1 OR NKNA OR TAC2 OR NKA.
 GN Oryctolagus cuniculus (Rabbit).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93371392; PubMed=8363593;
 RA Maegert H.J., Heiland A., Rose M., Forssmann W.G.;
 RT "Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.";
 RL Biochem. Biophys. Res. Commun. 195:128-131(1993).
 RN [2]
 RP SEQUENCE OF 72-92
 RA Kage R., McGregor G.P., Thim L., Conlon J.M.;
 RT "Gamma-neuropeptide K: a peptide isolated from rabbit gut that is
 derived from gamma-preprotachykinin.";
 RL Regul. Pept. 18:346-346(1987).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X62994; CAA44728.1; -
 DR PIR: S18922; S18922.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE: PS00267; TACHYKININ; 2.
 KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19 POTENTIAL.
 FT PEPTIDE 20 56 POTENTIAL.
 FT PEPTIDE 58 68 SUBSTANCE P.
 FT PEPTIDE 72 92 NEUROPEPTIDE GAMMA.
 FT PEPTIDE 83 92 NEUROKININ A.
 FT PEPTIDE 96 111 C-TERMINAL FLANKING PEPTIDE.
 FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD_RES 92 92 AMIDATION (G-93 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 115 AA; 13370 MW; 5EC767C9B10E1C6 CRC64;

Query Match 67.6%; Score 48; DB 1; Length 115;
 Best Local Similarity 81.8%; Pred. No. 1.4;
 Matches 9; Conservative 1; Mismatches 0; Gaps 0;
 QY 1 RPKPQPFGLM 11
 D6 58 RPKPQPFGLM 68
 |||||:|

RESULT 3
 TKNL_HUMAN

TKNL_HUMAN STANDARD; PRT; 129 AA.
 P20366; Q00072; O60600; O60601;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ I PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RX MEDLINE=87030957; PubMed=3770210;
 RA Hamar A.J., Armstrong A., Pascall J.C., Chapman K., Kosle R.,
 RA Curtis A., Goings J., Edwards C.R.W., Fink G.;
 RT "cDNA sequence of human beta-preprotachykinin, the common precursor
 to substance P and neurokinin A.";
 RL FEBS Lett. 208:67-72(1986).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC TISSUE=Brain;
 RA Tan A., Too H.P.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE=Testis;
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chwakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
 RA Ivell R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 human and mouse testis.";
 RL Endocrinology 128:2441-2448(1991).
 RN [4]
 RP SEQUENCE OF 98-107.
 RX MEDLINE=87275962; PubMed=3038549;
 RA Theodorsson-Norheim E., Joernvall H., Andersson M., Norheim I.,
 RA Oberg K., Jacobsson G.;
 RT "Isolation and characterization of neurokinin A, neurokinin A(3-10)
 and neurokinin A(4-10) from a neutral water extract of a metastatic
 ileal carcinoid tumour.";
 RL Eur. J. Biochem. 166:693-697(1987).
 RN [5]
 RP SEQUENCE OF 36-118 FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Blood, and Brain;
 RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
 RT "Identification of a delta isoform of preprotachykinin mRNA in human
 mononuclear phagocytes and lymphocytes.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 111-126.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=91133994; PubMed=2284201;
 RA McGregor G.P., Conlon J.M.;
 RT "Characterization of the C-terminal flanking peptide of human
 beta-preprotachykinin.";
 RL Peptides 11:907-910(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

Query Match 67.6%; Score 48; DB 1; Length 130;
 Best Local Similarity 81.8%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
 DB 58 RPKPQOWFFGLM 68

RESULT 5
 TKNL_MESAU STANDARD; PRT; 130 AA.
 ID TKNL_MESAU
 AC Q60341; P49110;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC STRAIN=AURA; TISSUE=Brain;
 RA Heitland A., Kruhoffer M., Juergen Maegert H.J., Forssmann W.G.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X80662; CAA56691.1; -;
 CC EMBL; X80663; CAA56692.1; -;
 CC InterPro; IPR003580; Protachykinin.
 CC InterPro; IPR002040; Tachykinin.
 CC Pfam; PF02202; Tachykinin; 1.
 CC ProDom; PD005598; Protachykinin; 1.
 CC SMART; SM00203; TK; 2.
 CC PROSITE; PS00267; TACHYKININ; 2.
 CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 CC Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19
 FT PROPEP 20 56
 FT PEPTIDE 58 68
 FT PEPTIDE 72 107
 FT PEPTIDE 72 73
 FT PEPTIDE 89 107
 FT PEPTIDE 98 107
 FT PEPTIDE 111 126
 FT MOD_RES 68 68
 FT MOD_RES 107 107
 FT VARSPLIC 74 88
 SQ SEQUENCE 130 AA; 14907 MW; CC92E9371A646F2E CRC64;

Query Match 67.6%; Score 48; DB 1; Length 130;

Best Local Similarity 81.8%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPKPQOWFWLM 11
 DB 58 RPKPQOWFFGLM 68

RESULT 6
 TKNL_MOUSE STANDARD; PRT; 130 AA.
 ID TKNL_MOUSE
 AC P41539; Q00073;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=ICR; TISSUE=Brain;
 RA Kato K., Muneoka E., Hosaka M., Murakami K., Nakayama K.;
 RT "Cloning and sequence analysis of mouse cDNAs encoding
 RT preprotachykinin A and B".
 RL Biomed. Res. 14:253-259(1993).
 RN [2]
 RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE=Brain;
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chiwakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
 RA Ivell R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 RT human and mouse testis".
 RL Endocrinology 128:2441-2448(1991).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D17584; BAA04508.1; -;
 CC EMBL; M68908; AAA39969.1; -;
 CC EMBL; M68909; AAA39970.1; -;
 CC MGD; MGI:98474; Tac1.
 CC InterPro; IPR003580; Protachykinin.
 CC InterPro; IPR002040; Tachykinin.
 CC Pfam; PF02202; Tachykinin; 1.
 CC ProDom; PD005598; Protachykinin; 1.
 CC SMART; SM00203; TK; 2.
 CC PROSITE; PS00267; TACHYKININ; 2.
 CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 CC Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19
 FT PROPEP 20 56
 FT PEPTIDE 58 68
 FT PEPTIDE 72 107
 FT PEPTIDE 72 73
 FT PEPTIDE 89 107
 FT PEPTIDE 98 107
 FT PEPTIDE 111 126
 FT MOD_RES 68 68
 FT MOD_RES 107 107
 FT VARSPLIC 74 88
 SQ SEQUENCE 130 AA; 14907 MW; CC92E9371A646F2E CRC64;

FT PEPTIDE 98 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 FT MOD.RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD.RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA).
 SQ SEQUENCE 130 AA; 15045 MW; 7BBDAL5FDE72FF8 CRC64;

Query Match 67.6%; Score 48; DB 1; Length 130;
 Best Local Similarity 81.8%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 |||||:| |
 Db 58 RPKPQQFFGLM 68

RESULT 7
 TKNL_RAT ID TKNL_RAT STANDARD; PRT; 130 AA.
 AC P06767; P08856; P22356;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
 RX MEDLINE=90331040; PubMed=1695945;
 RA Carter M.S., Krause J.E.;
 RT "Structure, expression, and some regulatory mechanisms of the rat
 RT preprotachykinin gene encoding substance P, neurokinin A,
 RT neuropeptide K, and neuropeptide gamma.";
 RL J. Neurosci. 10:2203-2214(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
 RX MEDLINE=87118268; PubMed=2433692;
 RA Krause J.E., Chirgwin J.M., Carter M.S., Xu Z.S., Hershey A.D.;
 RT "Three rat preprotachykinin mRNAs encode the neuropeptides substance
 RT P and neurokinin A.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:881-885(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=87025808; PubMed=2429656;
 RA Kawauchi Y., Hoshimaru M., Nawa H., Nakanishi S.;
 RT "Sequence analysis of cloned cDNA for rat substance P precursor:
 RT existence of a third substance P precursor.";
 RL Biochem. Biophys. Res. Commun. 139:1040-1046(1986).
 RL [4]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=87025808; PubMed=2429656;
 RA Kawauchi Y., Hoshimaru M., Nawa H., Nakanishi S.;
 RT "Sequence analysis of cloned cDNA for rat substance P precursor:
 RT existence of a third substance P precursor.";
 RL Biochem. Biophys. Res. Commun. 139:1040-1046(1986).
 RL [5]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=93192337; PubMed=8448217;
 RA Chapman K.E., Lyons V., Harman A.J.;
 RT "The sequence of 5' flanking DNA from the rat preprotachykinin gene;
 RT analysis of putative transcription factor binding sites.";
 RL Blochim. Biophys. Acta 1172:361-363(1993).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.

CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M34162; AAA41926.1;
 DR EMBL; M34159; AAA41926.1; JOINED.
 DR EMBL; M34160; AAA41926.1; JOINED.
 DR EMBL; M34161; AAA41926.1; JOINED.
 DR EMBL; M34184; AAA41925.1;
 DR EMBL; M34183; AAA41929.1;
 DR EMBL; M15191; AAA41928.1;
 DR EMBL; M14312; AAA41927.1;
 DR EMBL; L07328; AAA41924.1;
 DR EMBL; X56306; CAA39752.1;
 DR PIR; A26590; A26590.
 DR PIR; B26590; B26590.
 DR PIR; C26590; C26590.
 DR PIR; A37163; A37163.
 DR PIR; S12958; S12958.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE: PS00267; TACHYKININ; 2.
 KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 56 POTENTIAL.
 FT PEPTIDE 58 68 SUBSTANCE P.
 FT PEPTIDE 72 107 NEUROPEPTIDE K.
 FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 1ST PART.
 FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
 FT PEPTIDE 98 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 FT MOD.RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD.RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM
 FT VARSPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM
 FT VARSPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM
 FT VARSPLIC 130 AA; 15001 MW; B22EFE86DCCD75A CRC64;
 SQ SEQUENCE 130 AA; 15001 MW; B22EFE86DCCD75A CRC64;

Query Match 67.6%; Score 48; DB 1; Length 130;
 Best Local Similarity 81.8%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 |||||:| |
 Db 58 RPKPQQFFGLM 68

RESULT 8
 TKNA_CHICK ID TKNA_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204263; PubMed=2452461;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3] substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: JN0023; JN0023.
DR InterPro: IPR003560; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 II
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 63.4%; Score 45; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.44;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 RRPQQFFGLM 11
II:III:II

RESULT 9
CYB_RHOCA STANDARD; PRT; 436 AA.
ID CYB_RHOCA
AC P08502; P07057;
DC 01-APR-1988 (Rel. 07, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME B.
GN PEBT OR CYTB.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB1003;
RX MEDLINE=88011223; PubMed=2821268;
RA Davidson E., Daldal F.;
RT "Primary structure of the bcl complex of Rhodospseudomonas capsulata.
RT Nucleotide sequence of the pet operon encoding the Rieske cytochrome
RT b, and cytochrome c1 apoproteins.";
RL J. Mol. Biol. 195:13-24(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GA;
RX MEDLINE=86136096; PubMed=3004982;
RA Gabellini N., Sebald W.;
RT "Nucleotide sequence and transcription of the fbc operon from
RT Rhodospseudomonas sphaeroides. Evaluation of the deduced amino acid
RT sequences of the fbc protein, cytochrome b and cytochrome c1.";
RL Eur. J. Biochem. 154:569-579(1986).
RN [3]
RP CORRECTION OF ORGANISM GIVEN IN REF.2.
RX MEDLINE=88011233; PubMed=2821272;
RA Davidson E., Daldal F.;
RT "fbc operon, encoding the Rieske Fe-S protein cytochrome b, and
RT cytochrome c1 apoproteins previously described from Rhodospseudomonas
RT sphaeroides, is from Rhodospseudomonas capsulata.";

J. Mol. Biol. 195:25-29(1987).
[4]
RN MUTATIONS CONFERRING RESISTANCE TO QUINOL OXIDATION INHIBITORS.
RX MEDLINE=90076115; PubMed=2556259;
RA Daldal F., Tokito M.K., Davidson E., Faham M.;
RT "Mutations conferring resistance to quinol oxidation (Oz) inhibitors
RT of the cyt bcl complex of Rhodobacter capsulatus.";
RL EMBO J. 8:3951-3961(1989).
RN [5]
RP MUTAGENESIS.
RC STRAIN=WT1131;
RX MEDLINE=91105061; PubMed=2176897;
RA Robertson D.E., Daldal F., Dutton P.L.;
RT "Mutants of ubiquinol-cytochrome c2 oxidoreductase resistant to Qo
RT site inhibitors: consequences for ubiquinone and ubiquinol affinity
RT and catalysis.";
RL Biochemistry 29:11249-11260(1990).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS.
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X05630; CAA29117.1; -;
DR EMBL: X03476; CAA27195.1; -;
DR PIR: B29336; B29336.
DR PIR: S09373; S09373.
DR PIR: B25405; B25405.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c; 2.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE: PS00193; CYTOCHROME_B_QO; 1.
KW Electron transport; Respiratory chain; Heme; Transmembrane.
FT INIT_MET 0
FT METAL 96 96 IRON 1 (HEME B562 AXIAL LIGAND).
FT METAL 110 110 IRON 2 (HEME B566 AXIAL LIGAND).
FT METAL 197 197 IRON 2 (HEME B562 AXIAL LIGAND).
FT METAL 211 211 IRON 1 (HEME B566 AXIAL LIGAND).
FT VARIANT 66 67 MH -> ID (IN STRAIN GA).
FT VARIANT 280 280 V -> I (IN STRAIN GA).
FT MUTAGEN 143 143 F->L; S: LOSS OF BINDING AFFINITY
FT FOR UBIQUINONE AND UBIQUINOL.
SQ SEQUENCE 436 AA; 49218 MW; CIEAF62733087CA7 CRC64;

Query Match 62.0%; Score 44; DB 1; Length 436;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 359 RPKFRMFWFL 369
III:III:

RESULT 10
VEF_GVHA STANDARD; PRT; 902 AA.
ID VEF_GVHA
AC P54232;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation update)
 VIRAL ENHANCING FACTOR (VEF) (ENHANCIN) (104 KDA GLYCOPROTEIN)
 (SYNERGISTIC FACTOR).
 VEF.
 Heliothis armigera granulosis virus (HaGV) (Heliothis armigera
 granulovirus).
 Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 NCBI_TaxID=45440;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=96058802; PubMed=7595376;
 Roelink P.W., Corsaro B.G., Granados R.R.;
 "Characterization of the Helicoverpa armigera and Pseudaletia
 unipuncta granulovirus enhancer genes";
 J. Gen. Virol. 76:2693-2705(1995).
 CC -1- FUNCTION: INVOLVED IN DISRUPTION OF THE PERITROPHIC MEMBRANE AND
 CC FUSION OF NUCLEOCAPSIDS WITH MIDGUT CELLS (BY SIMILARITY).
 CC -1- SIMILARITY: TO TNGV AND PUGV VEF.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D28558; BAA05908.1; -
 CC Glycoprotein; Late protein.
 KW CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 782 782 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 840 840 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 902 AA; 104791 MW; D8E45BAA5F675FDE CRC64;
 Query Match 60.6%; Score 43; DB 1; Length 902;
 Best Local Similarity 70.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PKPQOWFWLM 11
 Db 353 PYPOIWAFLM 362
 RESULT 11
 DCHS_ENTAE STANDARD; PRT; 377 AA.
 AC P28577;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HISTIDINE DECARBOXYLASE (EC 4.1.1.22) (HDC).
 OS Enterobacter aerogenes (Aerobacter aerogenes).
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Enterobacter.
 CC NCBI_TaxID=548;
 CC [1]
 CC SEQUENCE FROM N.A.
 RP MEDLINE=91236707; PubMed=2033044;
 RA Kamath A.V., Vaaler G.L., Snell E.E.;
 RT "Pyridoxal phosphate-dependent histidine decarboxylases. Cloning,
 RT sequencing, and expression of genes from Klebsiella planticola and
 RT Enterobacter aerogenes and properties of the overexpressed enzymes";
 RL J. Biol. Chem. 266:19432-19437(1991).
 CC -1- CATALYTIC ACTIVITY: HISTIDINE = HISTAMINE + CO(2).
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DCHS, GAD, HDC AND
 CC TYRDC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M62745; AAA24802.1; -
 CC PIR: A40004; A40004.
 DR InterPro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; Pyridoxal_dec.1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC.1.
 KW Lyase; Decarboxylase; Pyridoxal phosphate.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT BINDING 232 232 PYRIDOXAL PHOSPHATE (POTENTIAL).
 SQ SEQUENCE 377 AA; 42303 MW; 4C7A3334ACA7D6AE CRC64;
 Query Match 59.2%; Score 42; DB 1; Length 377;
 Best Local Similarity 62.5%; Pred. No. 28;
 Matches 5; Conservative 1; Mismatches 2; Indels 1; Gaps 0;
 QY 2 PKPQOWFW 9
 Db 328 PKPSEWVM 335
 RESULT 12
 ATP8_SQUAC STANDARD; PRT; 55 AA.
 ID ATP8_SQUAC
 AC Q92250;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (ATPASE SUBUNIT 8) (A6L).
 GN MTATP8 OR ATP8.
 OS Squalus acanthias (Spiny dogfish).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
 OX NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99091711; PubMed=9873084;
 RA Rasmussen A.S., Arnason U.;
 RT "Phylogenetic studies of complete mitochondrial DNA molecules place
 RT cartilaginous fishes within the tree of bony fishes";
 RL J. Mol. Evol. 48:118-123(1999).
 CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
 CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Y18134; CAA77053.1; -
 DR InterPro: IPR001421; ATP-synt_8.
 DR Pfam: PF00895; ATP-synt_8.1.
 KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
 FT TRANSMEM 6 26 POTENTIAL.
 SQ SEQUENCE 55 AA; 6587 MW; 3FB9F843CEFA54EE CRC64;

Query Match 57.7%; Score 41; DB 1; Length 55;
Best Local Similarity 55.6%; Pred. No. 6.8;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQPOQFW 9
DB 44 KPAPEPNW 52

RESULT 13
CIW2_MOUSE STANDARD; PRT; 411 AA.
AC P97438;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM
DE CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TPKC1) (TREK-1 K+
DE CHANNEL SUBUNIT).
GN KCNK2.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=97157476; PubMed=9003761;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RT "Cloning, functional expression and brain localization of a novel
RT unconventional outward rectifier K+ channel.";
RL EMBO J. 15:6854-6862(1996).
RN [2]
RP REVISIONS.
RC TISSUE=Brain;
RX Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RA "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC HIPPOCAMPUS AND CEREBELLUM.
CC -!- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U73488; AAC53005.2; -
CC MGD: MGI:109366; Kcnk2.
CC InterPro: IPR003280; 2poreK_channel.
CC InterPro: IPR001622; Channel_pore_K.
CC InterPro: IPR000099; TWIK_channel.

DR PF02034; TWIK_channel; 1.
DR PRINTS; PRO1333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 POTENTIAL.
FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DD103EFA05 CRC64;

Query Match 56.3%; Score 40; DB 1; Length 411;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWM 11
DB 271 KPVWFWIL 279

RESULT 14
CIW2_HUMAN STANDARD; PRT; 426 AA.
AC O95069; QGUNE3;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING POTASSIUM
DE CHANNEL PROTEIN TREK-1) (TREK-1 K+ CHANNEL SUBUNIT) (TWO-PORE
DE POTASSIUM CHANNEL TPKC1).
GN KCNK2 OR TREK1 OR TREK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RA "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC


```
DR EMBL: AF129399; AAD47569.1; -.
DR EMBL: AF004711; AAD01203.1; -.
DR MIM: 603219; -.
DR InterPro: IPR003280; 2poreK_channel.
DR InterPro: IPR001622; Channel_pore_K.
DR InterPro: IPR000099; TWIK_channel.
DR Pfam: PF02034; TWIK_channel; 1.
DR PRINTS: PR01333; 2POREKCHANEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 82 POTENTIAL.
FT DOMAIN 144 170 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 193 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 253 283 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 288 308 POTENTIAL.
FT DOMAIN 309 426 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 378 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BY SIMILARITY).
FT DOMAIN 354 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 2 16 MISSING (IN REF. 2).
FT CONFLICT 309 311 RLV -> DWL (IN REF. 2).
FT CONFLICT 391 391 S -> N (IN REF. 2).
FT CONFLICT 411 411 A -> T (IN REF. 2).
SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;

Query Match 56.3%; Score 40; DB 1; Length 426;
Best Local Similarity 55.6%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWM 11
DB 286 KPLVWFWM 294

RESULT 15
CIWA_HUMAN STANDARD; PRT; 538 AA.
AC P57789; Q9HB59;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT).
GN KCNK10 OR TREK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20435789; PubMed=10880510;
RA Lesage F., Terrenoire C., Roney G., Lazdunski M.;
RT "Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple regulations by polyunsaturated fatty acids, lysophospholipids and Gs, Gi, and Gq protein-coupled receptors.";
RL J. Biol. Chem. 275:28398-28405(2000).
CC -I- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING UNSATURATED FREE FATTY ACIDS.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -I- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PANCREAS AND KIDNEY AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE.
CC -I- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
CC
```

```
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL: AF279890; AAG15191.1; -.
DR InterPro: IPR003280; 2poreK_channel.
DR InterPro: IPR001622; Channel_pore_K.
DR InterPro: IPR000099; TWIK_channel.
DR Pfam: PF02034; TWIK_channel; 1.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 72 92 POTENTIAL.
FT DOMAIN 154 180 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 POTENTIAL.
FT DOMAIN 263 294 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 299 319 POTENTIAL.
FT DOMAIN 320 338 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;

Query Match 56.3%; Score 40; DB 1; Length 538;
Best Local Similarity 55.6%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KPOQWFWM 11
DB 297 KPLVWFWM 305

Search completed: March 15, 2002, 14:32:19
Job time: 548 sec
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:23:47 ; Search time 34.92 Seconds
(without alignments)
23.995 Million cell updates/sec

Title: US-09-988-792-2

Perfect score: 71

Sequence: 1 RPKPQQWFWM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	67.6	11	1	SPHO	substance P - hors
2	48	67.6	11	1	A60654	substance P - guin
3	48	67.6	63	2	JC2412	tachykinin gamma c
4	48	67.6	72	2	I62742	tachykinin A gamma
5	48	67.6	72	2	JC5455	preprotachykinin-A
6	48	67.6	97	2	S12958	tachykinin delta p
7	48	67.6	112	1	SPRTA	substance P alpha
8	48	67.6	115	1	SPRBC	substance P gamma
9	48	67.6	115	2	S47039	tachykinin 1 precu
10	48	67.6	129	1	SPHOB	neurokinin 1 precu
11	48	67.6	130	1	SPRTB	substance P beta p
12	48	67.6	130	1	SPBOB	neurokinin 1 precu
13	48	67.6	130	2	S47038	tachykinin 1 precu
14	48	67.6	130	2	I52526	neurokinin 1 precu
15	45	63.4	111	2	JN0023	substance P - chic
16	45	63.4	453	2	F81720	lipid A biosynthes
17	45	63.4	455	2	E71569	probable acyltrans
18	44	62.0	437	1	B29336	ubiquinol--cytochr
19	43	60.6	365	2	C81050	cytochrome c oxida
20	43	60.6	365	2	F81826	probable cytochrom
21	42	59.2	378	1	A40004	histidine decarbox
22	41	57.7	55	2	T11538	H+-transporting AT
23	41	57.7	158	2	H70028	conserved hypothet
24	41	57.7	159	2	D71500	hypothetical prote
25	41	57.7	261	2	C83157	hypothetical prote
26	41	57.7	286	2	B82564	acetylcholan estera
27	41	57.7	291	1	S76015	hypothetical prote
28	41	57.7	304	2	A84353	acetyltransferase
29	41	57.7	529	2	S76167	hypothetical prote

ALIGNMENTS

RESULT 1

SPHO

substance P - horse

C:Species: Equus caballus (domestic horse)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C:Accession: A01558

R:Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A:Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pierdedarm.

A:Reference number: A01558

A:Accession: A01558

A:Molecule type: protein

A:Residues: 1-11 <STU>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; hormone

F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 67.6%; Score 48; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.096; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11

DB 1 RPKPQQWFWM 11

RESULT 2

A60654

substance P - guinea pig

C:Species: Cavia porcellus (guinea pig)

C:Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C:Accession: A60654

R:Murphy, R.

Neuropeptides 14, 105-110, 1989

A:Title: Primary amino acid sequence of guinea-pig substance P.

A:Reference number: A60654; MUID:90044685

A:Accession: A60654

A:Molecule type: protein

A:Residues: 1-11 <MUR>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 67.6%; Score 48; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.096; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11

DB 1 RPKPQQWFWM 11

```
RESULT 3
JC2412
tachykinin gamma chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: JC2412
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in the rat
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2412
A:Molecule type: mRNA
A:Residues: 1-63 <KHA>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:12-21/Product: substance P #status predicted <SUP>
F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
```

```
Query Match 67.6%; Score 48; DB 2; Length 63;
Best Local Similarity 81.8%; Pred. No. 0.54;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
    |||||:| |
Db 11 RPKPQQFFGLM 21

RESULT 4
I62742
tachykinin A gamma chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I62742; JC5453
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287
A:Accession: I62742
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-72 <RES>
A:Cross-references: GB:M68909; NID:9200469; PIDN:AAA39970.1; PID:g554261
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is involved in
C:Genetics:
A:Gene: gamma-PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>
```

```
Query Match 67.6%; Score 48; DB 2; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
    |||||:| |
Db 23 RPKPQQFFGLM 33

RESULT 5
JC5455
preprotachykinin-A gamma precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
C:Accession: JC5455; I45967
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287
```

```
A:Accession: JC5455
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-72 <CHI>
A:Cross-references: GB:M68912; NID:g163593; PIDN:AAA30725.1; PID:g552336
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is
C:Genetics:
A:Gene: ppt-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>
```

```
Query Match 67.6%; Score 48; DB 2; Length 42;
Best Local Similarity 81.8%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 RPKPQQWFWM 11
    |||||:| |
Db 23 RPKPQQFFGLM 33

RESULT 6
SI2958
tachykinin delta precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: SI2958; JC2413
R:Harmar, A.J.; Hyde, V.; Chapman, K.
FEBS Lett. 275, 22-24, 1990
A:Title: Identification and cDNA sequence of delta-preprotachykinin, a fourth splicing
A:Reference number: SI2958; MUID:91085565
A:Accession: SI2958
A:Molecule type: mRNA
A:Residues: 1-97 <KHA>
A:Cross-references: GB:X56306; NID:g55067; PIDN:CAA39752.1; PID:g56068
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2413
A:Molecule type: mRNA
A:Residues: 48-92 <KHA>
A:Cross-references: GB:S72369; NID:g632805; PIDN:AAB31499.1; PID:g632806
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:59-68/Product: substance P #status predicted <SUP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
```

```
Query Match 67.6%; Score 48; DB 2; Length 97;
Best Local Similarity 81.8%; Pred. No. 0.82;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
    |||||:| |
Db 58 RPKPQQFFGLM 68

RESULT 7
SPRTA
substance P alpha precursor - rat
N:Alternate names: preprotachykinin alpha
N:Contains: substance P
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: B26590
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Heisler, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the tripeptides substance P and ne
A:Reference number: A94187; MUID:87110268
A:Accession: B26590
```

A;Molecule type: mRNA
 A;Residues: 1-112 <KRA>
 A;Cross-references: GB:M34184; NID:g206329; PIDN:AAA41925.1; PID:g206330
 C;Comment: Alternative splicing of the mRNA for substance P precursor yields the alpha 4
 C;Comment: The alpha form is processed to yield substance P.
 C;Superfamily: substance P precursor
 C;Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
 F;1-112/Product: substance P alpha precursor #status predicted <PREA>
 F;1-15/Domain: signal sequence #status predicted <SIG>
 F;58-68/Product: substance P #status predicted <SBP>
 F;68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 67.6%; Score 48; DB 1; Length 112;
 Best Local Similarity 81.8%; Pred. No. 0.95;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 DB 58 RPKPQQFFGLM 68

RESULT 8
 SPRBG

substance P gamma precursor - rabbit
 N;Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykinin
 N;Contains: neurokinin A; neuropeptide K; substance P
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
 C;Accession: JN0709; A60302; A60200; S18922
 C;Maegert, H.J.; Heitland, A.; Rose, M.; Forssmann, W.G.
 Biochem. Biophys. Res. Commun. 195, 128-131, 1993
 A;Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.
 A;Reference number: JN0709; MUID:93371392
 A;Accession: JN0709

A;Molecule type: mRNA
 A;Residues: 1-115 <MA2>
 A;Cross-references: EMBL:X62994; NID:gl565; PIDN:CAA44728.1; PID:gl566
 R;Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
 Regul. Pept. 18, 346, 1987

A;Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived from
 A;Reference number: A60302
 A;Accession: A60302
 A;Molecule type: protein
 A;Residues: 72-92 <KAG>
 R;Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
 J. Neurochem. 50, 1412-1417, 1988

A;Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived fr
 A;Reference number: A60200; MUID:88199570
 A;Accession: A60200

A;Molecule type: protein
 A;Residues: 72-92 <KA2>
 C;Comment: The gamma alternatively spliced form is processed to yield substance P and ne
 C;Superfamily: substance P precursor

F;1-15/Domain: signal sequence #status predicted <SIG>
 F;58-68/Product: substance P #status predicted <SBP>
 F;72-92/Product: gamma-neuropeptide K #status experimental <NPX>
 F;83-92/Product: neurokinin A #status predicted <NKA>
 F;68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
 F;92/Modified site: amidated carboxyl end (Met)

Query Match 67.6%; Score 48; DB 1; Length 115;
 Best Local Similarity 81.8%; Pred. No. 0.97;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 DB 58 RPKPQQFFGLM 68

RESULT 9

S47039
 tachykinin 1 precursor - golden hamster
 C;Species: Mesocricetus auratus (golden hamster)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C;Accession: S47039
 R;Heitland, A.; Kruhoffer, M.; Juergen Maegert, H.J.; Forssmann, W.G.
 submitted to the EMBL Data Library, July 1994
 A;Reference number: S47038
 A;Accession: S47039
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-115 <HEI>
 A;Cross-references: EMBL:X80663; NID:g520938; PIDN:CAA56692.1; PID:g520939
 C;Superfamily: substance P precursor

Query Match 67.6%; Score 48; DB 2; Length 115;
 Best Local Similarity 81.8%; Pred. No. 0.97;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
 DB 58 RPKPQQFFGLM 68

RESULT 10
 SPUBH

neurokinin 1 precursor, beta splice form [validated] - human
 N;Alternate names: neurokinin A; neurokinin alpha; neuromedin , neuropeptide K; prep
 N;Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 pre
 C;Species: Homo sapiens (man)
 C;Date: 12-Feb-1988 #sequence_revision 26-May-1995 #text_change 19-May-2000
 C;Accession: A24805; A60425; S00069; S03033; JC5451; JC5450; A59269; A59270; B59270;
 R;Harmar, A.J.; Armstrong, A.; Pascall, J.C.; Chapman, K.; Rosie, R.; Curtis, A.; Goll
 FEBS Lett. 208, 67-72, 1986

A;Title: cDNA sequence of human beta-preprotachykinin, the common precursor to substa
 A;Reference number: A24805; MUID:87030957

A;Accession: A24805

A;Molecule type: mRNA

A;Residues: 1-129 <HAR>

A;Cross-references: GB:M28109; EMBL:X54469; NID:g29482; PIDN:CAA38351.1; PID:g29483

R;McGregor, G.P.; Conlon, J.M.

Peptides 11, 907-910, 1990

A;Title: Characterization of the C-terminal flanking peptide of human beta-preprotach

A;Reference number: A60425; MUID:91133994

A;Accession: A60425

A;Molecule type: protein

A;Residues: 111-126 <MCG>

A;Experimental source: Neuroendocrine tumor of adrenal medulla

R;Theodorsson-Norheim, E.; Joernvall, H.; Andersson, M.; Norheim, I.; Oberg, K.; Jac

Eur. J. Biochem. 166, 693-697, 1987

A;Title: Isolation and characterization of neurokinin A, neurokinin A(3-10) and neuro

A;Reference number: S00069; MUID:87275962

A;Accession: S00069

A;Molecule type: protein

A;Residues: 98-107 <THE>

R;Kage, R.; Thim, L.; Creutzfeldt, W.; Conlon, J.M.

Biochem. J. 253, 203-207, 1988

A;Title: Post-translational processing of preprotachykinins. isolation of protachykin

A;Reference number: S03033; MUID:88339887

A;Accession: S03033

A;Molecule type: protein

A;Residues: 20-30 <KAG>

R;Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwell, R.

Endocrinology 128, 2441-2448, 1991

A;Title: tachykinin (substance-P) gene expression in Leydig cells of the human and mo

A;Reference number: JC5450; MUID:91209287

A;Accession: JC5451

A;Status: translation not shown; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 36-73, 89-122 <CHIL>

A;Cross-references: GB:M68907; NID:gl90292; PIDN:AAA60160.1; PID:g553619

A;Accession: JC5450

A:Reference number: A37163; MUID:90331040
A:Accession: A37163
A:Molecule type: DNA
A:Residues: 1-130 <CAR>
A:Cross-references: GB:M34159; GB:M34160; GB:M34162; NID:g206334; PIDN:AAA41926.1; PID:9206342; GB:M35277
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neuropeptide Y
A:Reference number: A94187; MUID:87118268
A:Accession: A26590
A:Molecule type: mRNA
A:Residues: 1-130 <KRA>
A:Cross-references: GB:M15191; NID:g206341; PIDN:AAA41928.1; PID:g206342; GB:M35277
A:Accession: C26590
A:Molecule type: mRNA
A:Residues: 1-73,89-130 <KR2>
A:Cross-references: GB:M34183; NID:g206343; PIDN:AAA41929.1; PID:g206344
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of two isoforms
A:Reference number: A25067; MUID:87025808
A:Accession: A25067
A:Molecule type: mRNA
A:Residues: 1-73,89-130 <KAW>
A:Cross-references: GB:M14312; NID:g206339; PIDN:AAA41927.1; PID:g206340
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in rat brain
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2411
A:Molecule type: mRNA
A:Residues: 48-110 <KHA>
A:Experimental source: intestine
C:Comment: Alternative splicing of the mRNA for substance P, precursor yields the beta and gamma forms
C:Comment: The beta and gamma forms are processed to yield substance P and neurokinin B
C:Genetics:
A: Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C: Superfamily: substance P precursor
C: Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F: 1-130/Product: substance P beta precursor #status predicted <PRE>
F: 1-73,89-130/Product: substance P gamma precursor #status predicted <PREG>
F: 1-15/Domain: signal sequence #status predicted <SIG>
F: 58-68/Product: substance P #status predicted <SBP>
F: 98-107/Product: neurokinin A #status predicted <NKA>
F: 68/Modified site: amidated carboxyl end (Met) (amide in mature form from following)
F: 107/Modified site: amidated carboxyl end (Met) (amide in mature form from following)

```

QY      1 RPKPQQWFWM 11
      |||||:|:|
Db      58 RRPQPFEGLM 68

RESULT  12
SPBOB
N:Altkinate names: neurokinin A; preprotachykinin; substance A, substance P
N:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 pre
C:Species: Bos primigenius taurus (cattle)
C:date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change: 16-Jun-2000
C:Accession: A05093; A01557; B25067; A61460; JC5454; 14,966
R:Nawa, H.; Kotani, H.; Nakanishi, S.
Nature 312, 729-734, 1984
A:title: Tissue-specific generation of two preprotachykinin mRNAs from one gene by al
A:reference number: A05093; MUID:85086245
A:Accession: A05093
A:Molecule type: DNA
A:Residues: 1-130 <NAWI>
A:cross-references: GB:X02351; GB:M14786; NID:g655; PIDN:CAA4a206.1; PID:g11q7197

```

R:Nawa, H.; Hirose, T.; Takashima, H.; Inayama, S.; Nakanishi, S.
Nature 306, 32-36, 1983
A:Title: Nucleotide sequences of cloned cDNAs for two types of bovine brain substance P
A:Reference number: A93318; MUID:84039802
A:Accession: A01559
A:Molecule type: mRNA
A:Residues: 1-130 <NAW2>
A:Cross-references: GB:X00075; NID:g758; PIDN:CAA24939.1; PID:g759
A:Accession: A01557
A:Molecule type: mRNA
A:Residues: 1-96, 'M', 116-130 <NAW3>
A:Cross-references: GB:X00076; NID:g762; PIDN:CAA24942.1; PID:g763
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of a
A:Reference number: A25067; MUID:87025808
A:Accession: B25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
R:McGregor, G.P.; Kage, R.; Thim, L.; Conlon, J.M.
J. Neurochem. 53, 1871-1877, 1989
A:Title: Quantitation and characterization of peptides from the C-terminal flanking region
A:Reference number: A61460; MUID:90039314
A:Accession: A61460
A:Molecule type: protein
A:Residues: 111-126 <MCG>
A:Experimental source: corpus striatum
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwells, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5454
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-120, 'A', 122 <CHI>
A:Cross-references: GB:M68911; NID:g163591; PIDN:AAA30724.1; PID:g552335
C:Comment: The protein is processed to produce neurokinin 1 (substance P) and neurokinin
C:Genetics:
A:Gene: PPT-A
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
A:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
F:1-130/Product: neurokinin 1 precursor, beta splice form #status predicted <SP>
F:1-96, 'M', 116-130/Product: neurokinin 1 precursor, alpha splice form #status predicted
F:1-73, 89-130/Product: neurokinin 1 precursor, gamma splice form #status predicted <SP>
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status experimental <SBP>
F:111-126/Domain: neurokinin 2 #status predicted <NEK>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 67.6%; Score 48; DB 1; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPQQWFWM 11
Db 58 RPKPQQQFFGLM 68
RESULT 13
S47038
tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47038
R:Heitland, A.; Kruhoffer, M.; Juergen Maegert, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47038

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <HEI>
A:Cross-references: EMBL:X80662; NID:g520917; PIDN:CAA56691.1; PID:g520918
C:Superfamily: substance P precursor

Query Match 67.6%; Score 48; DB 2; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 58 RPKPQQQFFGLM 68

RESULT 14
152526

neurokinin 1 precursor - mouse
N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N:Contains: neurokinin 1; neurokinin 2
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000
C:Accession: I52526; JC5452; I62741
R:Kako, K.; Muneke, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A:Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and
A:Reference number: I52526
A:Accession: I52526
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-130 <KAK>
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwells, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5452
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 36-122 <CHI>
A:Cross-references: GB:M68908; NID:g200467; PIDN:AAA39969.1; PID:g554260
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status predicted <NK1>
F:98-107/Product: neurokinin 2 #status predicted <NK2>
F:111-126/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 67.6%; Score 48; DB 2; Length 130;
Best Local Similarity 81.8%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 58 RPKPQQQFFGLM 68

RESULT 15
JN0023

substance P - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C:Accession: JN0023
R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A:Reference number: JN0023; MUID:88204263

A:Accession: JN0023

A:Molecule type: protein

A:Residues: 1-11 <CON>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match

Best Local Similarity 63.4%; Score 45; DB 2; Length 11;

Matches 8; Conservative 72.7%; Pred. No. 0.28;

Mismatches 2; Indels 1; Gaps 0;

QY 1 RPKPQQQFWLM 11

II:III:II

Db 1 RRPQQOFFGLM 11

Search completed: March 15, 2002, 14:23:48

Job time: 222 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:22:27 ; Search time 66.25 Seconds
(without alignments)
12.299 Million cell updates/sec

Title: US-09-988-792-2

Perfect score: 71

Sequence: 1 RPKQQWFWM 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	11	4 AAP30142	Sequence of peptid
2	71	100.0	11	9 AAP80317	Sequence of neurop
3	71	100.0	11	19 AAW50969	Substance P analog
4	71	100.0	11	20 AAW52656	Human tachykinin a
5	71	100.0	11	22 AAB98881	Chimeric analgesic
6	71	100.0	11	22 AAB91413	Tachykinins peptid
7	71	100.0	12	22 AAB98882	Chimeric analgesic
8	68	95.8	11	5 AAP40479	Substance P analog
9	68	95.8	11	9 AAP80313	Sequence of neurop
10	68	95.8	11	9 AAP80314	Sequence of neurop
11	68	95.8	11	11 AAR05856	D-arginine 1, D-pr

12	68	95.8	11	12 AAR11144	Substance P analog
13	68	95.8	11	19 AAW50966	Substance P analog
14	68	95.8	11	19 AAW50958	Substance P analog
15	68	95.8	11	20 AAW92657	Human tachykinin a
16	68	95.8	11	22 AAB91434	Tachykinins peptid
17	68	95.8	24	13 AAR28680	Galanin(1-12)-pro-
18	68	95.8	24	22 AAB92023	Galanin peptide SE
19	68	95.8	24	22 AAB92031	Galanin peptide SE
20	66	93.0	11	16 AAW09004	Spantide analogue,
21	66	93.0	11	20 AAW99690	Substance P analog
22	66	93.0	11	20 AAW99691	Substance P analog
23	61	85.9	11	9 AAP80315	Sequence of neurop
24	61	85.9	11	19 AAW50968	Substance P analog
25	61	85.9	11	22 AAB98879	Chimeric analgesic
26	61	85.9	11	22 AAB91412	Tachykinins peptid
27	61	85.9	12	22 AAB98880	Chimeric analgesic
28	60	84.5	11	5 AAP40481	Substance P analog
29	60	84.5	11	9 AAP80316	Sequence of neurop
30	60	84.5	11	19 AAW50979	Substance P analog
31	60	84.5	11	19 AAW50972	Substance P analog
32	60	84.5	11	19 AAW50942	Substance P antago
33	60	84.5	11	21 AAB08303	Amino acid sequenc
34	60	84.5	11	22 AAB91414	Tachykinins peptid
35	57	80.3	11	21 AAB08313	Amino acid sequenc
36	54	76.1	8	9 AAP80322	Sequence of neurop
37	54	76.1	8	19 AAW50970	Substance P analog
38	51	71.8	11	13 AAR28392	Bradykinin recepto
39	50	70.4	11	4 AAP30141	Sequence of peptid
40	49	69.0	11	13 AAR21934	Substance P [Tyr7]
41	49	69.0	11	13 AAR28443	Neurokinine 1 liga
42	49	69.0	11	20 AAW92666	Human tachykinin a
43	48	67.6	8	9 AAP80318	Sequence of neurop
44	48	67.6	8	12 AAR15359	Substance P antago
45	48	67.6	8	19 AAW50974	Substance P analog

ALIGNMENTS

RESULT 1
AAP30142
ID AAP30142 standard; Protein; 11 AA.
XX
AC AAP30142:
DT 14-JUN-1992 (first entry)
XX
DE Sequence of peptides with substance P inhibiting activity.
XX
KW Substance P antagonist; pain therapy; hypertension.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /label= D-P
FT Modified-site 7 /label= D-W
FT Misc-difference 8 /label= F,I
FT Modified-site 9 /label= D-W
FT Modified-site 11 /label= M,I
FT /note= "bonded to NH2"
XX
PN W08301251-A.
XX
PD 14-APR-1983.
XX
PP 09-OCT-1981; 81WO-DE00171.
XX
PR 09-OCT-1981; 81WO-DE00171.
XX
PR 09-OCT-1981; 81EP-0902802.

PA (FERR) FERRING ARZNEIMITTE.
PA (HORI/) HORIG J.

XX Horig J;

XX WPI; 1983-39155K/16 (39155K).

XX Undeca-peptide derivs. with substance P inhibiting activity -
PT useful for treating pain and hypertension

XX Claim 2; Page 18; 25pp; German.

XX The peptides of the invention are powerful antagonists of Substance
CC pain and so are useful in human and veterinary medicine, for treating
CC pain and hypertension (esp.) chronic conditions. A 10 microm concn.
CC of the peptide produced about 50% inhibition at a Substance P concn. of
CC 7.5-20 nanom.

XX Sequence 11 AA;

Query Match 100.0%; Score 71; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQWFWM 11
Db 1 rpkpqgfwlm 11

RESULT 2

AAP80317
ID AAP80317 standard; protein; 11 AA.

XX AAP80317;

XX 14-SEP-1990 (first entry)

XX Sequence of neuropeptide antagonist E which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist E.

XX Swiss 3T3 cells.

XX Key Location/Qualifiers

FT Misc-difference 2

FT /label=OTHER

FT /note="DPro"

FT Misc-difference 7

FT /label=OTHER

FT /note="DTrp"

FT Misc-difference 9

FT /label=OTHER

FT /note="DTrp"

FT Misc-difference 11

FT /label=OTHER

FT /note="Met-NH2"

PN W08807551-A.

XX 06-OCT-1988.

XX 31-MAR-1988; 88WO-GB00255.

XX 25-NOV-1987; 87GB-0027638.

XX (IMCR) IMPERIAL CANCER RES.

PA Rosengurt E, Zachary I, Woll P;

XX

XX

XX

XX

XX

XX

XX

XX

DR WPI; 1988-292842/41.

XX New polypeptide receptor for bombesin type polypeptides(s)

PT is isolated from surface of Swiss 3T3 cells, and antibodies and

PT antagonists are useful for treating uncontrolled cell proliferation

XX Disclosure; Table 2; 42pp; English.

XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.

XX Sequence 11 AA;

Query Match 100.0%; Score 71; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.5e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQWFWM 11

Db 1 rpkpqgfwlm 11

RESULT 3

AAW50969
ID AAW50969 standard; peptide; 11 AA.

XX AAW50969;

XX 31-JUL-1998 (first entry)

XX Substance P analogue, [D-Pro2,D-Trp7,9].

XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KW spantide.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2

FT /note= "D-form residue"

FT Misc-difference 7

FT /note= "D-form residue"

FT Misc-difference 9

FT /note= "D-form residue"

FT Modified-site 11

FT /note= "C-terminal amide"

XX EP835662-A2.

XX 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

XX 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

PA

XX Jaggi M, Mukherjee R;
 XX WPI; 1998-208959/19.
 XX Composition containing analogues of vasoactive intestinal peptide,
 PT somatostatin - bombesin and substance P, for treatment of tumours
 PT and for inhibiting over-expression of these peptide(s)
 XX Disclosure; Page 13; 49pp; English.
 XX The invention relates to a new composition which comprises: (i) the
 CC somatostatin analogue SOM2 AGCKNFFdWKPTSDC (3-14 disulphide bridge),
 CC and (ii) at least 4 of the peptides: antagonist of vasoactive
 CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
 CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
 CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
 CC more general compositions containing peptide analogues of somatostatin,
 CC VIP, bombesin and substance P. The compositions are used in human or
 CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
 CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
 CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
 CC breast, kidney or particularly rectum and colon, and (b) to prevent,
 CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
 CC cells express receptors for VIP, somatostatin, bombesin and/or substance
 CC P. The present sequence represents a substance P analogue.
 XX Sequence 11 AA;

Query Match 100.0%; Score 71; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.5e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFWLM 11
 Db 1 rpkpqgfwlm 11

RESULT 4
 AAW92656
 ID AAW92656 standard; peptide; 11 AA.
 AC AAW92656;
 DT 30-APR-1999 (first entry)
 XX Human tachykinin agonist beta-amyloid peptide fragment #2.
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiopathy.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 XX US5876948-A.
 PN 02-MAR-1999.
 PD 27-JUL-1991; 91US-0737371.
 XX 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;
 XX WPI; 1999-189630/16.
 XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX Disclosure; Column 11-12; 28pp; English.
 XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
 CC with amyloidosis and non-inherited congenital angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX Sequence 11 AA;

Query Match 100.0%; Score 71; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.5e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFWLM 11
 Db 1 rpkpqgfwlm 11

RESULT 5
 AAB98881
 ID AAB98881 standard; Peptide; 11 AA.
 AC AAB98881;
 DT 14-AUG-2001 (first entry)
 XX Chimeric analgesic peptide #37.
 DE Opioid receptor binding; nociceptive receptor binding; analgesic;
 KW pain; chimeric peptide.
 KW Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /label= OTHER
 FT /note= "C-terminal amide"
 XX WO200130371-A2.
 PN 03-MAY-2001.
 PD 27-OCT-2000; 2000WO-US29789.
 XX 28-OCT-1999; 99US-0428692.
 PR (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
 PI WPI; 2001-397593/42.
 XX New chimeric peptides used for treating pain comprise opioid receptor

PT binding group and nociceptive receptor binding group
 PS Claim 10; Page 16; 34pp; English.
 XX
 CC The present invention describes a number of chimeric peptides comprising
 CC an opioid receptor binding moiety and a nociceptive receptor binding
 CC moiety. These can be used as analgesics for the treatment of pain. Unlike
 CC opioid receptor based peptides alone, tolerance does not result from
 CC their long-term use. The present sequence is one of the peptides of the
 CC invention.
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 71; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.5e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
 |||||
 Db 1 rpkpqgfwlm 11

RESULT 6
 AAB91413
 ID AAB91413 standard; Peptide; 11 AA.
 XX
 AC AAB91413;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Tachykinins peptide SEQ ID NO:589.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 XX WPI; 2001-112059/12.
 DR
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 XX
 XX Disclosure; Page 392; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (iii) and a
 CC reactive group (ii) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (iv), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB97441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 71; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.5e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
 |||||
 Db 1 rpkpqgfwlm 11

RESULT 7
 AAB98882
 ID AAB98882 standard; Peptide; 12 AA.
 XX
 AC AAB98882;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Chimeric analgesic peptide #38.
 XX
 KW Opioid receptor binding; nociceptive receptor binding; analgesic;
 KW pain; chimeric peptide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 12 /note= "D-form residue"
 FT Modified-site 12 /label= OTHER
 FT /note= "C-terminal amide"

XX WO200130371-A2.
 XX
 XX 03-MAY-2001.
 XX
 XX 27-OCT-2000; 2000WO-US29789.
 XX
 XX 28-OCT-1999; 99US-0428692.
 XX
 XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 XX
 XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
 XX
 XX WPI; 2001-397593/42.
 XX
 XX New chimeric peptides used for treating pain comprising opioid receptor
 XX binding group and nociceptive receptor binding group
 XX
 XX Claim 10; Page 16; 34pp; English.

CC The present invention describes a number of chimeric peptides comprising
 CC an opioid receptor binding moiety and a nociceptive receptor binding
 CC moiety. These can be used as analgesics for the treatment of pain. Unlike
 CC opioid receptor based peptides alone, tolerance does not result from
 CC their long-term use. The present sequence is one of the peptides of the
 CC invention.
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 71; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQWFWM 11
 Db 1 rpkpqqgfwl 11

RESULT 8
 AAP40479
 ID AAP40479 standard; peptide; 11 AA.
 XX AC AAP40479;
 XX AC
 DT 27-NOV-1991 (first entry)
 XX Substance P analogue.
 DE Substance P; analogue; antiinflammatory agent; analgesic.
 XX US4481139-A.
 XX 06-NOV-1984.
 XX 13-APR-1983; 83US-0484646.
 XX 13-APR-1983; 83US-0484646.
 XX (UYTE-) UNIVERSITY OF TEXAS SYSTEM.
 XX Folkers K, Ji-cheng X;
 XX WPI; 1984-294258/47.
 XX Peptide analogues of substance P - useful as antagonists, e.g. as
 PT antiinflammatory agents and analgesics.
 XX Claim 1; page 5; 5pp; English.
 XX The peptide is a D-Arg1, D-Trp7, D-Trp9, Leu11 analogue of substance
 CC P. the peptide is a substance P antagonist with higher activity than
 CC known substance P analogues. It may be used as a biological
 CC research tool, ophthalmological antiinflammatory agent and analgesic.
 XX Sequence 11 AA;

Query Match 95.8%; Score 68; DB 5; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.00024;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQWFWM 11
 Db 1 rpkpqqgfwl 11

RESULT 9
 AAP80313
 ID AAP80313 standard; protein; 11 AA.
 XX AC AAP80313;
 XX AC
 DT 14-SEP-1990 (first entry)
 XX Sequence of neuropeptide antagonist A which binds with polypeptide
 DE receptor for bombesin type polypeptides.
 DE Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
 XX cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
 KW antagonist A.
 XX

OS Swiss 3T3 cells.
 XX Key Location/Qualifiers
 FH Misc-difference 1 /label=OTHER
 FT /note="DArg"
 FT Misc-difference 2 /label=OTHER
 FT /note="DPro"
 FT Misc-difference 7 /label=OTHER
 FT /note="DTrp"
 FT Misc-difference 9 /label=OTHER
 FT /note="Dtrp"
 FT Misc-difference 11 /label=OTHER
 FT /note="Leu-NH2"
 XX WO8807551-A.
 XX 06-OCT-1988.
 XX 31-MAR-1988; 88WO-GB00255.
 XX 25-NOV-1987; 87GB-0027638.
 XX (IMCR) IMPERIAL CANCER RES.
 XX Rosengurt E, Zachary I, Woll P;
 XX WPI; 1988-292842/41.
 XX New polypeptide receptor for bombesin type polypeptide(s) -
 PT is isolated from surface of Swiss 3T3 cells, and antibodies and
 PT antagonists are useful for treating uncontrolled cell proliferation
 XX Disclosure; Table 2; 42pp; English.
 XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
 CC cells which binds selectively with polypeptides of the bombesin type and
 CC binds with antagonist A and antagonist D. Antagonist A is a
 CC commercially available structural variant of substance P, known as
 CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
 CC [D-Pro2] spantide. Antagonist B is also commercially available structural
 CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
 CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
 CC substance P antagonists (see AAP80313-80322) were tested for their
 CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
 CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
 CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
 CC potent than either A or D. Spantide (B) had no antagonist activity even
 CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
 CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
 CC growth is associated with disorders of proteins of the bombesin family.
 XX Sequence 11 AA;

Query Match 95.8%; Score 68; DB 9; Length 11,
 Best Local Similarity 90.9%; Pred. No. 0.00024;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQQWFWM 11
 Db 1 rpkpqqgfwl 11

RESULT 10
 AAP80314
 ID AAP80314 standard; protein; 11 AA.
 XX AC AAP80314;

XX 14-SEP-1990 (first entry)
 XX Sequence of neuropeptide antagonist B which binds with polypeptide
 DE receptor for bombesin type polypeptides.
 XX
 KW Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
 KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
 KW antagonist B.
 XX
 XX Swiss 3T3 cells.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1 /label=OTHER
 FT /note="DArg"
 FT
 FT Misc-difference 7 /label=OTHER
 FT /note="DTrp"
 FT Misc-difference 1 /label=OTHER
 FT /note="DTrp"
 FT Misc-difference 14 /label=OTHER
 FT /note="Leu-NH2"
 FT
 XX W08807551-A.
 XX
 XX 06-OCT-1988.
 XX
 XX 31-MAR-1988; 88WO-GB00255.
 XX
 XX 25-NOV-1987; 87GB-0027638.
 XX
 XX (IMCR) IMPERIAL CANCER RES.
 XX
 XX Rosengurt E, Zachary I, Woll P;
 XX
 XX WPI; 1988-292842/41.
 XX
 XX New polypeptide receptor for bombesin type polypeptide(s) -
 PT is isolated from surface of Swiss 3T3 cells, and antibodies and
 PT antagonists are useful for treating uncontrolled cell proliferation
 XX
 XX Disclosure; Table 2; 42pp; English.
 XX
 XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
 CC cells which binds selectively with polypeptides of the bombesin type and
 CC binds with antagonist A and antagonist D. Antagonist A is a
 CC commercially available structural variant of substance P, known as
 CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
 CC [D-Pro2] spantide. Antagonist B is also commercially available structural
 CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
 CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
 CC substance P antagonists (see AAP80313-80322) were tested for their
 CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
 CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
 CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
 CC potent than either A or D. Spantide (B) had no antagonist activity even
 CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
 CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
 CC growth is associated with disorders of proteins of the bombesin family.
 XX
 XX Sequence 11 AA;

Query Match 95.8%; Score 68; DB 9; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.00024;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RPKPQOWFWLM 11
 Db 1 rpkpqowfwll 11

RESULT 11
 AAR05856
 ID AAR05856 standard; protein; 11 AA.
 XX
 AC AAR05856;
 XX
 DT 07-SEP-1990 (first entry)
 XX
 DE D-arginine 1, D-proline 2, D-tryptophan 7,9, Leucine 11;
 DE -substance P angiotensin antagonist.
 XX
 KW Angiotensin; ectopic hormone; mas oncogene; cancer;
 KW neuroblastoma; neuroendocrine.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label=Dextrorotatory form.
 FT Modified-site 2 /label=Dextrorotatory form.
 FT Modified-site 7 /label=Dextrorotatory form.
 FT Modified-site 9 /label=Dextrorotatory form.
 FT Modified-site /label=Dextrorotatory form.
 FT
 XX W09003181-A.
 XX
 XX 05-APR-1990.
 XX
 XX 22-SEP-1989; 89WO-0001121.
 XX
 XX 24-SEP-1988; 88GB-0022483.
 XX
 XX (MEDI-) MED RES COUNCIL.
 XX
 XX Hanley MR, Goedert M;
 XX
 XX WPI; 1990-132106/17.
 XX
 XX Use of substances which block the activity of angiotensin -
 PT for the treatment or prevention of tumour development or ectopic
 PT hormone prodn.
 XX
 XX Claim 8; Page 19; 23pp; English.
 XX
 CC Peptide blocks biological activity of angiotensin and is active
 CC against the mas oncogene, retarding tumour growth, esp
 CC neuroendocrine and neuroblastoma tumours.
 XX
 SQ Sequence 11 AA;
 Query Match 95.8%; Score 68; DB 11; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.00024;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RPKPQOWFWLM 11
 Db 1 rpkpqowfwll 11

RESULT 12
 AAR11144
 ID AAR11144 standard; Protein; 11 AA.
 XX
 AC AAR11144;
 XX
 DT 21-MAY-1991 (first entry)
 XX
 DE Substance P analogue.

XX Anti-proliferation agent; neurogenetic inflammation; fibroblasts;
KW agonist.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /label= D-Arg
FT Modified-site 7 /label= D-Trp
FT Modified-site 9 /label= D-Trp
FT Modified-site 9.10 /label= non-peptide bond
FT Modified-site /note= "Trp-L(CH2NH)-Trp"
FT Modified-site 11 /label= Nle
XX W09102745-A.
XX
XX 07-MAR-1991.
XX
XX 16-AUG-1990; 90WO-US04633.
XX
XX 16-AUG-1989; 89US-0394727.
XX (TULA) TULANE E FUND ADMINISTRA.
XX
XX Coy DH, Moreau JP;
XX WPI; 1991-087240/12.
XX
XX Modified linear peptide analogue of natural substance P - acts as
PT competitive inhibitor of substance P and is used for treating
PT neuro genetic inflammation and as anti-proliferative agent.
XX
XX Claim 11; Page 34; 40pp; English.
XX
XX The peptide has a non-peptide bond introduced between Trp9 and
CC Leu10. This may alternatively be positioned between Leu10 and
CC Nle11. For prep., a benzhydrylamine resin was coupled to Boc-Leu.
CC Boc-Leu aldehyde was dissolved in 5 ml DMF and added to the resin
CC TFA salt suspension followed by addn. of NACNBH3 and stirring for
CC one hour. The remaining amino acids were then coupled successively.
CC In tests the peptide inhibited P-stimulated amylase release from
CC pancreatic acini
CC See also AAR11143.
XX
XX Sequence 11 AA;

Query Match 95.8%; Score 68; DB 12; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPQQWFWM 11
Db 1 rpkpqgwfll 11

RESULT 13
AAW50966
ID AAW50966 standard; peptide; 11 AA.
XX AAW50966;
XX
XX 31-JUL-1998 (first entry)
XX Substance P analogue, spantide I.
XX
XX vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KW

KW spantide.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX EP835662-A2.
XX
XX 15-APR-1998.
XX
XX 11-DEC-1996; 96EP-0309012.
XX
XX 08-OCT-1996; 96US-0727679.
XX 16-AUG-1996; 96IN-0001822.
XX (NAIM-) NAT INST IMMUNOLOGY.
XX Jaggi M, Mukherjee R;
XX WPI; 1998-208959/19.
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX
XX Disclosure; Page 13; 49pp; English.
XX
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFFDWKPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); Vip receptor-binding inhibitor (VIP2); Vip
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue, spantide I.
XX
XX Sequence 11 AA;

Query Match 95.8%; Score 68; DB 19; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 rpkpqgwfll 11

RESULT 14
AAW50958
ID AAW50958 standard; peptide; 11 AA.
XX AAW50958;
XX
XX 31-JUL-1998 (first entry)
XX
XX Substance P analogue, [D-Arg1,D-Pro2,D-Trp7,9,Leu11]-substance P.
XX

KW vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor.
XX Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT
XX

PN EP835662-A2.

XX 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

PR 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

XX Jaggi M, Mukherjee R;

PI WPI; 1998-208959/19.

XX Composition - bombesin and substance P, for treatment of tumours

PT and for inhibiting over-expression of these peptide(s)

XX Disclosure; Page 12; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the

CC somatostatin analogue SOM2 AGCKNFEDWKTPTSDC (3-14 disulphide bridge),

CC and (ii) at least 4 of the peptides: antagonist of vasoactive

CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP

CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin

CC antagonist (BOM1) and substance P antagonist (SPL). Also claimed are

CC more general compositions containing peptide analogues of somatostatin,

CC VIP, bombesin and substance P. The compositions are used in human or

CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour

CC or cancer cells, particularly for treatment of leukaemia, lymphoma,

CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,

CC breast, kidney or particularly rectum and colon, and (b) to prevent,

CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer

CC cells express receptors for VIP, somatostatin, bombesin and/or substance

CC P. The present sequence represents a substance P analogue.

XX Sequence 11 AA;

SQ

Query Match 95.8%; Score 68; DB 19; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.00024;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWM 11

Db 1 rpkpqwfwm 11

RESULT 15

AAW92657

ID AAW92657 standard; peptide: 11 AA.

XX AAW92657;

XX 30-APR-1999 (first entry)

XX

DE

XX

KW

KW

XX

OS

XX

XX

FH

FT

FT

FT

FT

FT

FT

XX

PN

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Human tachykinin agonist beta-amyloid peptide fragment #3.

Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

Alzheimer's disease; Down's syndrome; amyloidosis; human;

hereditary cerebral haemorrhage; non-inherited conophilic angiopathy.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 1 /note= "D-form residue"

Misc-difference 7 /note= "D-form residue"

Misc-difference 9 /note= "D-form residue"

Misc-difference 11 /note= "D-form residue"

US5876948-A.

02-MAR-1999.

27-JUL-1991; 91US-0737371.

29-JUL-1991; 91US-0737371.

27-JUL-1990; 90US-0559173.

(CHIL-) CHILDRENS MEDICAL CENT.

Yankner BA;

WPI; 1999-189630/16.

Screening for neurotoxin inhibitors - by testing compounds for their

effect on beta-amyloid peptide neurotoxic effect on neuronal cells

Disclosure; Column 11-12; 28pp; English.

This invention describes a method for screening compounds for inhibiting a neurotoxin. The method involves incubating tachykinin agonists with neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease, Down's syndrome, and the syndromes of hereditary cerebral haemorrhage with amyloidosis and non-inherited conophilic angiopathy with cerebral haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human beta-amyloid peptide fragments.

Sequence 11 AA;

Query Match

Best Local Similarity 95.8%; Score 68; DB 20; Length 11;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPQQWFWM 11

Db 1 rpkpqwfwm 11

Search completed: March 15, 2002, 14:22:27

Job time: 367 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:23:05 : Search time 32.16 seconds
(without alignments)
7.697 Million cell updates/sec

Title: US-09-988-792-2
Perfect score: 71
Sequence: 1 RPKPQQWFWM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued_Patents_AA.*
- 1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2.6/ptodata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2.6/ptodata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2.6/ptodata/2/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	11	5441935-5	Patent No. 5441935
2	68	95.8	11	5441935-2	Patent No. 5441935
3	61	85.9	11	5441935-3	Patent No. 5441935
4	54	76.1	8	5441935-10	Patent No. 5441935
5	49	69.0	11	2 US-07-737-371E-12	Sequence 12, Appl
6	48	67.6	8	5441935-6	Patent No. 5441935
7	48	67.6	11	US-07-934-553-1	Sequence 1, Appl
8	48	67.6	11	US-08-184-935-12	Sequence 12, Appl
9	48	67.6	11	US-08-269-288-2	Sequence 2, Appl
10	48	67.6	11	US-08-338-484-1	Sequence 1, Appl
11	48	67.6	11	US-08-175-432-1	Sequence 1, Appl
12	48	67.6	11	US-08-225-474-1	Sequence 1, Appl
13	48	67.6	11	US-08-391-910-2	Sequence 2, Appl
14	48	67.6	11	US-08-418-994-2	Sequence 2, Appl
15	48	67.6	11	US-08-480-505-3	Sequence 3, Appl
16	48	67.6	11	US-08-391-814-2	Sequence 2, Appl
17	48	67.6	11	US-08-167-870-1	Sequence 1, Appl
18	48	67.6	11	US-08-255-272-6	Sequence 6, Appl
19	48	67.6	11	US-08-441-591-6	Sequence 6, Appl
20	48	67.6	11	US-08-303-362A-6	Sequence 6, Appl
21	48	67.6	11	US-08-462-859A-1	Sequence 1, Appl
22	48	67.6	11	US-08-123-659A-1	Sequence 1, Appl
23	48	67.6	11	US-08-462-415-2	Sequence 2, Appl
24	48	67.6	11	US-08-463-874-2	Sequence 2, Appl
25	48	67.6	11	US-08-464-247A-1	Sequence 1, Appl
26	48	67.6	11	US-08-464-248A-1	Sequence 1, Appl
27	48	67.6	11	US-08-444-135-2	Sequence 2, Appl

28	48	67.6	11	1 US-08-318-391-2	Sequence 2, Appl
29	48	67.6	11	2 US-08-796-598-11	Sequence 11, Appl
30	48	67.6	11	2 US-08-447-175A-11	Sequence 11, Appl
31	48	67.6	11	2 US-07-737-371E-21	Sequence 21, Appl
32	48	67.6	11	2 US-07-737-371E-22	Sequence 22, Appl
33	48	67.6	11	2 US-07-737-371E-24	Sequence 24, Appl
34	48	67.6	11	2 US-07-737-371E-27	Sequence 27, Appl
35	48	67.6	11	2 US-07-737-371E-65	Sequence 65, Appl
36	48	67.6	11	2 US-07-737-371E-77	Sequence 77, Appl
37	48	67.6	11	2 US-08-848-766A-1	Sequence 1, Appl
38	48	67.6	11	3 US-08-927-128-17	Sequence 17, Appl
39	48	67.6	11	4 US-08-257-966-2	Sequence 2, Appl
40	48	67.6	11	5 PCT-US95-05600-23	Sequence 23, Appl
41	48	67.6	11	6 5441935-1	Patent No. 5441935
42	48	67.6	11	6 5441935-8	Patent No. 5441935
43	48	67.6	12	1 US-08-441-591-7	Sequence 7, Appl
44	48	67.6	12	1 US-08-303-362A-7	Sequence 7, Appl
45	48	67.6	12	4 US-08-505-250-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
5441935-5
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO:5:
; LENGTH: 11
5441935-5

Query Match 100.0%; Score 71; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 RPKPQQWFWM 11
Db 1 RPKPQQWFWM 11

RESULT 2
5441935-2
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO:2:
; LENGTH: 11
5441935-2

Query Match 95.8%; Score 68; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0001;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Caps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | |
Db 1 RPKPQQWFWM 11

RESULT 3

5441935-3
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 3:
; LENGTH: 11
5441935-3

Query Match 85.9%; Score 61; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | |
Db 1 RPKPQQWFWM 11

RESULT 4

5441935-10
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 10:
; LENGTH: 8
5441935-10

Query Match 76.1%; Score 54; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQQWFWM 11
| | | | | | | |
Db 1 PQQWFWM 8

RESULT 5

US-07-737-371E-12
; Sequence 12, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-12

Query Match 69.0%; Score 49; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.072;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | |
Db 1 RPKPQQYFGLM 11

RESULT 6

5441935-6
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO: 6:
; LENGTH: 8
5441935-6

Query Match 67.6%; Score 48; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWM 11
| | | | | | | |
Db 1 PQQWFWM 8

RESULT 7

US-07-934-553-1

; Sequence 1, Application US/07934553
; Patent No. 5314690
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, ROY
; APPLICANT: HARRIS, KATHLEEN E
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING Ige
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT
; STREET: 100 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,553
; FILING DATE: 19920821
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,071
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTRESS, SUSAN B
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET INFORMATION: NU-9033CIP
; TELEPHONE: 312/456-8000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-934-553-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWLM 11
| | | | | | | | | | | |
Db 1 RPKPQQQFFGLM 11

RESULT 8
US-08-184-935-12
; Sequence 12, Application US/08184935
; Patent No. 5476770
; GENERAL INFORMATION:
; APPLICANT: PRADELES, PHILIPPE
; TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN
; TITLE OF INVENTION: OR HAPTEN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,935
; FILING DATE: 24-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NO. 5476770man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 846-286-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "C-terminal amide"
; US-08-184-935-12

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWLM 11
| | | | | | | | | | | |
Db 1 RPKPQQQFFGLM 11

RESULT 9
US-08-269-288-2
; Sequence 2, Application US/08269288
; Patent No. 5491140
; GENERAL INFORMATION:
; APPLICANT: Bruns, Robert F.
; APPLICANT: Gehlert, Donald R.
; APPLICANT: Howbert, James J.
; APPLICANT: Lunn, William H.W.
; TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,288
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9715
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-269-288-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 10

US-08-338-484-1
Sequence 1, Application US/08338484
Patent No. 5494926

GENERAL INFORMATION:

APPLICANT: Owens, Andrew P.
APPLICANT: Teall, Martin R.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: 2/3-(HETEROCYCLIC ALKYL
TITLE OF INVENTION: AMINO)-1-(SUBSTITUTED PHENYL-METHOXY)-ETHANES/PROPANES AS
TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Robert J. No. 5494926th
STREET: 126 E. Lincoln Ave., P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,484
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: No. 5494926th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-484-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 11

US-08-175-432-1
Sequence 1, Application US/08175432
Patent No. 5495047

GENERAL INFORMATION:

APPLICANT: Saari, Walfred S.
APPLICANT: Van Niel, Monique B.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: FUSED TRICYCLIC COMPOUNDS,
PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE
TITLE OF INVENTION: IN THERAPY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NORTH, ROBERT J.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,432
FILING DATE: 07-JAN-1994

CLASSIFICATION: 560
ATTORNEY/AGENT INFORMATION:
NAME: No. 5495047th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1152Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-175-432-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 12

US-08-225-474-1
Sequence 1, Application US/08225474
Patent No. 5560915

GENERAL INFORMATION:

APPLICANT: Patterson, Roy
APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: Ige Mediated Allergies
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 S. Wacker Drive, Suite 960
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000
TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-225-474-1

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 13
US-08-391-910-2
Sequence 2, Application US/08391910
Patent No. 5563133
GENERAL INFORMATION:
APPLICANT: Hipskind, Philip A.
TITLE OF INVENTION: HEXAMETHYLENEMINYL TACHYKININ RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,910
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9979
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-910-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 14
US-08-418-994-2
Sequence 2, Application US/08418994
Patent No. 5565568
GENERAL INFORMATION:
APPLICANT: Cho, Sung-Yong S.
APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, J. J.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: 2-ACYLAMINOPROPANAMIDES AS TACHYKININ
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,994
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-8252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-418-994-2

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
Db 1 RPKPQQFFGLM 11

RESULT 15
US-08-480-505-3
Sequence 3, Application US/08480505

; Patent No. 5601821
; GENERAL INFORMATION:
; APPLICANT: STANWORTH, DENIS R
; APPLICANT: LEWIN, IAN V
; APPLICANT: NAYVAR, SARITA
; APPLICANT: JONES, VALERIE
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-3360
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,505
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,692
; FILING DATE:
; APPLICATION NUMBER: US 07/776,380
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: GB 8913737.6
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB90/00926
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 875-0400
; TELEFAX: (703) 525-3468
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Neuropeptide "Substance P"
; US-08-480-505-3

Query Match 67.6%; Score 48; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFGLM 11
|||||:||
Db 1 RPKPQOWFGLM 11

Search completed: March 15, 2002, 14:23:06
Job time: 216 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:29:47 ; Search time 352.97 Seconds
(without alignments)
8.653 Million cell updates/sec

Title: US-09-988-792-2
Perfect score: 71
Sequence: 1 RPKQQWFWM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues
Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main: *
1: /cgn2_6/ptodata/2/paa/PTCUS_COMB.pcp.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pcp.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pcp.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pcp.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pcp.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pcp.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pcp.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pcp.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pcp.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pcp.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pcp.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pcp.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pcp.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pcp.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pcp.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pcp.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pcp.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pcp.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pcp.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pcp.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pcp.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pcp.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pcp.*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	11	18	US-09-428-692-36
2	71	100.0	11	20	US-09-657-276-589
3	71	100.0	12	18	US-09-428-692-37
4	68	95.8	11	20	US-09-657-276-610
5	68	95.8	24	20	US-09-657-276-1199
6	68	95.8	24	20	US-09-657-276-1207
7	61	85.9	11	18	US-09-428-692-34
8	61	85.9	11	20	US-09-657-276-588
9	61	85.9	12	18	US-09-428-692-35

10	60	84.5	11	20	US-09-657-276-590	Sequence 590, Appl
11	49	69.0	11	3	US-07-737-371A-12	Sequence 12, Appl
12	49	69.0	11	3	US-07-737-371D-12	Sequence 12, Appl
13	48	67.6	8	3	US-07-672-300A-9	Sequence 9, Appl
14	48	67.6	11	3	US-07-618-504A-2	Sequence 2, Appl
15	48	67.6	11	3	US-07-670-039A-2	Sequence 2, Appl
16	48	67.6	11	3	US-07-705-071-1	Sequence 1, Appl
17	48	67.6	11	3	US-07-737-371A-21	Sequence 21, Appl
18	48	67.6	11	3	US-07-737-371A-22	Sequence 22, Appl
19	48	67.6	11	3	US-07-737-371A-24	Sequence 24, Appl
20	48	67.6	11	3	US-07-737-371A-27	Sequence 27, Appl
21	48	67.6	11	3	US-07-737-371A-66	Sequence 66, Appl
22	48	67.6	11	3	US-07-737-371D-21	Sequence 21, Appl
23	48	67.6	11	3	US-07-737-371D-22	Sequence 22, Appl
24	48	67.6	11	3	US-07-737-371D-24	Sequence 24, Appl
25	48	67.6	11	3	US-07-737-371D-27	Sequence 27, Appl
26	48	67.6	11	3	US-07-737-371D-65	Sequence 65, Appl
27	48	67.6	11	3	US-07-877-675A-5	Sequence 5, Appl
28	48	67.6	11	5	US-08-102-875-2	Sequence 2, Appl
29	48	67.6	11	5	US-08-119-244-2	Sequence 2, Appl
30	48	67.6	11	5	US-08-119-244-3	Sequence 3, Appl
31	48	67.6	11	5	US-08-153-847-2	Sequence 2, Appl
32	48	67.6	11	5	US-08-171-134-2	Sequence 2, Appl
33	48	67.6	11	6	US-08-235-401-2	Sequence 2, Appl
34	48	67.6	11	6	US-08-259-266-2	Sequence 2, Appl
35	48	67.6	11	7	US-08-307-741-2	Sequence 2, Appl
36	48	67.6	11	7	US-08-307-741-3	Sequence 3, Appl
37	48	67.6	11	7	US-08-343-750-2	Sequence 2, Appl
38	48	67.6	11	7	US-08-387-056-2	Sequence 2, Appl
39	48	67.6	11	8	US-08-401-394-2	Sequence 2, Appl
40	48	67.6	11	8	US-08-401-394A-2	Sequence 2, Appl
41	48	67.6	11	8	US-08-408-238-2	Sequence 2, Appl
42	48	67.6	11	10	US-08-680-004-17	Sequence 17, Appl
43	48	67.6	11	12	US-08-844-462-11	Sequence 11, Appl
44	48	67.6	11	16	US-09-265-690B-3	Sequence 3, Appl
45	48	67.6	11	19	US-09-597-737A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-428-692-36
; Sequence 36, Application US/09428692
; GENERAL INFORMATION:
; APPLICANT: Carr et al.
; TITLE OF INVENTION: NOVEL CHIMERIC ANALGESIC PEPTIDES
; FILE REFERENCE: 18475-016
; CURRENT APPLICATION NUMBER: US/09/428,692
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-428-692-36

Query Match 100.0%; Score 71; DB 18; Length 11.
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKQQWFWM 11
| | | | | | | | | |
Db 1 RPKQQWFWM 11

RESULT 2
US-09-657-276-589
; Sequence 589, Application US/09657276

; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 589
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-589

Query Match 100.0%; Score 71; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
| | | | | | | | | |
Db 1 RPKPOQWFWM 11

RESULT 3
US-09-428-692-37
; Sequence 37, Application US/09428692
; GENERAL INFORMATION:
; APPLICANT: Carr et al.
; TITLE OF INVENTION: NOVEL CHIMERIC ANALGESIC PEPTIDES
; FILE REFERENCE: 18475-016
; CURRENT APPLICATION NUMBER: US/09/428,692
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-428-692-37

Query Match 100.0%; Score 71; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
| | | | | | | | | |
Db 1 RPKPOQWFWM 11

RESULT 4
US-09-657-276-610
; Sequence 610, Application US/09657276
; GENERAL INFORMATION:

; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 610
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-610

Query Match 95.8%; Score 68; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0063;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQWFWM 11
| | | | | | | | | |
Db 1 RPKPOQWFWM 11

RESULT 5
US-09-657-276-1199
; Sequence 1199, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1199
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1199

Query Match 95.8%; Score 68; DB 20; Length 24;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | |
DB 14 RPKPQQWFWM 24

RESULT 6
US-09-657-276-1207
; Sequence 1207, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibault, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1207
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1207

Query Match 95.8%; Score 68; DB 20; Length 24;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | |
DB 14 RPKPQQWFWM 24

RESULT 7
US-09-428-692-34
; Sequence 34, Application US/09428692
; GENERAL INFORMATION:
; APPLICANT: Carr et al.
; TITLE OF INVENTION: NOVEL CHIMERIC ANALGESIC PEPTIDES
; FILE REFERENCE: 18475-016
; CURRENT APPLICATION NUMBER: US/09/428,692
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-428-692-34

Query Match 85.9%; Score 61; DB 18; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.063;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | |
DB 1 RPKPQQWFWM 11

RESULT 8
US-09-657-276-588
; Sequence 588, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibault, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 588
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-588

Query Match 85.9%; Score 61; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.063;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQWFWM 11
| | | | | | | | | |
DB 1 RPKPQQWFWM 11

RESULT 9
US-09-428-692-35
; Sequence 35, Application US/09428692
; GENERAL INFORMATION:
; APPLICANT: Carr et al.
; TITLE OF INVENTION: NOVEL CHIMERIC ANALGESIC PEPTIDES
; FILE REFERENCE: 18475-016
; CURRENT APPLICATION NUMBER: US/09/428,692
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-428-692-35

Query Match 85.9%; Score 61; DB 18; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.068;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
|||||:||||
Db 1 RPKPQOWFWLM 11

RESULT 10

US-09-657-276-590
; Sequence 590, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjughem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaut, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 590
; LENGTH: 11
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-590

Query Match 84.5%; Score 60; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.088;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
|||||:||||
Db 1 RPKPQOWFWLM 11

RESULT 11

US-07-737-371A-12
; Sequence 12, Application US/07737371A
; GENERAL INFORMATION:
; APPLICANT: Bruce A. Yanker
; TITLE OF INVENTION: TACHYKININ AGONISTS FOR
; TITLE OF INVENTION: TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371A

; FILING DATE: July 29, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/599,172
; FILING DATE: July 27, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-07-737-371A-12

Query Match 69.0%; Score 49; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQOWFWLM 11
|||||:||||
Db 1 RPKPQOWFWLM 11

RESULT 12

US-07-737-371D-12
; Sequence 12, Application US/07737371D
; GENERAL INFORMATION:
; APPLICANT: Yanker, Bruce A.
; TITLE OF INVENTION: SUBSTANCE P AND TACHYKININ
; TITLE OF INVENTION: AGONISTS FOR TREATMENT OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371D
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/599,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371D-12

Query Match 69.0%; Score 49; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRPQQWFWM 11
| | | | | | | | | | | | | |
Db 1 RRPQQYFGLM 11

RESULT 13
US-07-672-300A-9
; Sequence 9, Application US/07672300A
; GENERAL INFORMATION:
; APPLICANT: Dr. Romano Deghenghi
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5"
; COMPUTER: Hewlett Packard (IBM PC Compatible)
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/672,300A
; FILING DATE: 19910320
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Harry C. Jones III
; REGISTRATION NUMBER: 20,280
; REFERENCE/DOCKET NUMBER: 7264-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-790-9090
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: Yes

US-07-672-300A-9

Query Match 67.6%; Score 48; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 2.9e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQWFWM 11
| | | | | | | | | | | | | |
Db 1 PQQWFWM 8

RESULT 14
US-07-618-504A-2
; Sequence 2, Application US/07618504A
; GENERAL INFORMATION:
; APPLICANT: HOESS, RONALD H
; APPLICANT: O BRIEN, JOHN P
; APPLICANT: SALEMM, FRANCIS R
; TITLE OF INVENTION: STRUCTURAL PROTEINS FROM
; ARTIFICIAL GENES

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
; ADDRESSEE: DU PONT COMPANY
; STREET: BARLEY MILL PLAZA 36/2116
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: USA
; ZIP: 19880-0036
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/618,504A
; FILING DATE: 19901128
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SIEGELL, BARBARA C
; REFERENCE/DOCKET NUMBER: CR 8895
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-892-7949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-618-504A-2

Query Match 67.6%; Score 48; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRPQQWFWM 11
| | | | | | | | | | | | | |
Db 1 RRPQQYFGLM 11

RESULT 15
US-07-670-039A-2
; Sequence 2, Application US/07670039A
; GENERAL INFORMATION:

APPLICANT: Gerard, Norma P.
; TITLE OF INVENTION: CONTROLLING NK-1 RECEPTOR-
; TITLE OF INVENTION: MEDIATED RESPONSES AND RELATED
; TITLE OF INVENTION: DIAGNOSTICS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/670,039A
; FILING DATE: 19910315
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 00108/062001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-670-039A-2

Query Match 67.6%; Score 48; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQQFWLM 11
|||||:|
Db 1 RPKPQQQFFGLM 11

Search completed: March 15, 2002, 14:29:47
Job time: 531 sec